

## FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG  
AGCAGCTCCTGCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA  
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT  
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT  
GTCCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCC  
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC  
CGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG  
GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG  
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG  
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC  
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG  
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG  
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT  
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC  
TCCTGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTTC  
CTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGG  
CTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTC  
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCTCCTC  
CCCTTCCCTCGGGAGGGTCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT  
CCACCCCTGGCTACCCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA  
GCTGAGGGAAGGTACGAGTTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC  
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAA  
CGTGAAAGGGCGGCCGCGACTCT  
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT  
TACAAAT

## **FIGURE 2**

MTDSPPPGHPPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV  
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC  
GAAICQPPCRNGGSCVQPGRRCRCPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCW  
EGHSLSADGTLCVPKGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLAS  
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 93-97, 270-274

### **N-myristoylation sites.**

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,  
191-197, 265-271

### **Amidation site.**

amino acids 26-30

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 152-164

### **Cell attachment sequence.**

amino acids 130-133

### **EGF-like domain cysteine pattern signature.**

amino acids 123-135

### FIGURE 3

CGCTCGCCCCGTCGCCCCCTCGCCTCCCCGCAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG  
GTCAGCCCACGGCGGGGACTATGGTGAAATTCGCGGCGCTCACGCACTACTGGCCCCCTGATC  
CGGTTCTTGGTGCCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA  
CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT  
ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCCTGGTGTTT  
GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCTGTGTATGGTGGTGGCAGGGGCCATCGC  
TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC  
ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCCCTTT  
CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAAACACAAATACAGTTT  
CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTTGTAGCCATTTTGC  
TTCACAGTCACCTGGAATGCCGGGAGCCCCCTGCTCATCCCGATCCTCTCCTTGTACATGGGC  
GCACTTGTGCGCTGCACCACCTGTGCCTGGGCTACTACAAGAACATTACAGCATCATCCC  
TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT  
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG  
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC  
ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGAGTGGACTTTGCCTTTGCAGAAC  
TCTGTGTTGTTCCCTTTGCGGATCTTCTCCTTCTTCCCAGTTCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCTTGCCCCAGCTCTGTGCTGCG  
GATCATCGTCCTCATCGCCAGCCTCGTGGTCTTACCCTACCTGGGGGTGCACGGTGCAGCCC  
TGGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGGTGCCTATCGCTGCG  
TGCTATGTCTACCGGAAGCAGAAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA  
CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGG  
AGAATGAATTAAGGCACGGGACGCCATGGGCAGTGCAGGGACGGTCAGTCAGGATGACACTTC  
GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTTTTTGTGTTTTGTTTGGTAAT  
GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT  
GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAACAAACGAAACAACTGAC  
TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC  
TCTCCCCCTGGACAATCTCCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT  
CACCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG  
TTAAAACCTCGGCTTCCTTTGATTGCTTCCAGTCACATGGCCGTACAAAGAGATGGAGCCC  
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG  
GAGGCGGGTGGCACGCTGCAGCCCGAGTCCCCGTTCACACTGAGGAACGGAGACCTGTGAC  
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCCGGG  
GGCAGCAAACCTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCCTAGATCTGAGCAA  
GCTGTCACTTCTACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTACAAAA  
GCGCATCTCCAGATTCCAGACCCTGCCGCATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC  
CTTTCCTGAAGGTCGCATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTT  
TACAGTGAACCTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC  
TTTTGAAGTAGATATATTACCTGGTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA  
TTGAGAATGTACTACGGTACTTCCCTCCCACACCATAACGATAAAGCAAGACATTTTATAACG  
ATACCAGAGTCACTATGTGGTCTCCTGAAATAACGCATTTCGAAATCCATGCAGTGCAGTA  
TATTTTTCTAAGTTTTTGAAAGCAGGTTTTTTTCTTTAAAAAAATATAGACACGGTTCACT  
AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA  
TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCTATTTTCG  
ATTTTCAATAAAATGTCTCTAATACAAAAA

## **FIGURE 4**

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF  
TGPMSDFKNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYIIINKLHHVDES  
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC  
REPLLIPILSLYMGALVRCTTLC LGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL  
ATQORISRPVNL FVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNPSN  
KLVSTSN TVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVvPLR  
IFSFFPV PVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLG VHGATLGVGSL  
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPPTEEVTDIVEMREENE

### **Transmembrane domains:**

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,  
408-423, 431-445

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## **FIGURE 5**

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT  
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG  
ACAAGAATAACCCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC  
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
TCTGTGTTGTTCCCTTTGCGGATCTTCTCCTTCTTCCAGTTCCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

109101"44584660

## **FIGURE 6**

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG  
GAGCAGGGCAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC  
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT  
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCCTTTGCGGATTTTCT  
CCTTTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG  
AAAACCTTTGTCCTTGCCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT  
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCTCCTGGCGGGCA

109101"44582650

## **FIGURE 7**

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA  
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT  
CCTACCCTACCTGGGGGTGCACGGTGAGAC

09978544.101601

## FIGURE 8

GCCCCGCGCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA  
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG  
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCC  
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG  
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG  
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT  
TCTTTTTTACCCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG  
AATGGGTTTTGGTTCTTTAAGTTCTTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT  
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCTGTGGGCTCCTTCCTCTTCA  
TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC  
AAGGCCGAGGAGTGCGATTCCCGTGCCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT  
CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTAAGTCTGAGCCCAGCGGCT  
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT  
GCTGTCTGCCCCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCTAT  
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA  
ACCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG  
ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT  
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC  
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC  
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT  
GGCCTCACTGCACGTATGATGACGCTACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA  
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC  
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGGCAGCCT  
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACT  
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTG  
CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA  
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCCTTCCCCTCCTCCCTGT  
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGG  
CTGCTGGAGAGAGCGGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT  
CCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT  
AAGACTTTTTCTAATAAACAAGCCAGTGCGTGTAATAAAAAA

## **FIGURE 9**

MGACLGACSLLSASCCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE  
SOLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSW  
NQRWLGKAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC  
VCVSIAAVLPKVQDAQPNISGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA  
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA  
ACEGRAFDNEQDGVITYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICAS  
WAGLLLYLWTLVAPLLLRNRDFS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

04582660

## FIGURE 10

GAGCGAGGCCGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTG  
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA  
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGC  
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG  
TGACTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC  
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG  
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG  
TGTATGGGGGAATACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTTATCATAACCGGTTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT  
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG  
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAATTGCAGGA  
GCTGTCACGGGAAGTCTTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT  
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG  
GTGAGACTGTTTCAAGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACCTGGAA  
GAGTGGAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC  
CTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAAACTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC  
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGCTTTTTCTTTCTT  
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT  
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA  
GCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

109707-4458660

## **FIGURE 11**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF  
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDVQSAH  
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR  
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE  
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-24

#### **Transmembrane domains:**

amino acids 76-96 and 171-195

#### **N-glycosylation site:**

amino acids 153-156

109707 14532660

## **FIGURE 12**

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA  
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT  
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTCGTTTCATG  
GCTGGCGCCGAACC



## **FIGURE 13**

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT  
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGTCTGCCGAAGCTGTGACTGCCGAT  
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG  
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGGTGTATGGGGGA  
ATACCAGCTTTTATTTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA  
TAACC

097544-10101  
T09T0T"445B/660



## **FIGURE 15**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALV  
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQR  
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVVGIGLFFSFTEILGVWL  
TYRYRNQKDPRANPSAFL

### **Signal Peptide:**

amino acids 1-34

### **Transmembrane domains:**

amino acids 47-63, 72-95 and 162-182

0997544-1060  
T09T0T-44882660

## **FIGURE 16**

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTTATATGATTATTCTGTAANT  
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG  
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA  
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA  
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC  
TACAGATACAGGAACCAG

0597544.10103  
"TTTTT" 44532660

## **FIGURE 17**

AATCCCAAATTCCCCAATTTTTTTGGNCTTTTATAGGGAAAGATGTGTTGTGGTAAAAAGTGT  
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG  
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG  
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGAT  
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC  
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCTTGC

## **FIGURE 18**

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTTAGCCC  
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC  
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA  
TCATAGGAGAATATGC

## FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG  
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT  
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT  
TCCAGGTCAAGGCCTACACTTTTCACTGAACCCTTCCACCTGATTGTGTCTATGACTGGCTG  
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC  
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC  
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCCTACCAC  
TGCAGTGGCATCTTCCAGAGCCCTGGTCTTGGGATCCAGAAACAGCATCTGTTGTGGCTAT  
CACAGTCCAAGAAGTGTTCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG  
CAGGAAGCCCCATGACCCTGAGTTGTGAGACAAAGTTGCCCCCTGCAGAGGTCAGCTGCCCGC  
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT  
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCTACTGGTGTGAGGCAGCCACTGAGG  
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT  
GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCTGA  
GGAGGGCCCCCTGGGCCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT  
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG  
CAGGATGTGAGAGTCTCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA  
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAAGTAAACAGTTCATCCATGATCTCACT  
TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGTCTGCACATATGCATAAGTA  
CTTTTACAAGTTGTCCCAGTGTTTTGTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTT  
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC  
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA  
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA  
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTGGGGGATGGTGGGATGT  
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG  
GGCAGTACCCCAACGAAAAATAATCTGGCCCAAATGTGAGTTGTACTGAGTTTGAGAAA  
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT  
TATCTCTTTCCAGCCTCATTGAGCTATTCTTACTGACATAACAGTCTTTAGCTGGTGCTATG  
GTCTGTTCTTTAGTTCTAGTTTGTATCCCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC  
AAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC  
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT  
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCACAAAAACAGCTGTGCCAAACACCG  
ACTCTGTGCTTGCCTTGATCTTGAACCTTCCAGCCTCCAGAACTATGAGAAATAAAATCTGG  
TTGTTTGTAGCCTAA

## **FIGURE 20**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGVWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV  
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQCQAWQDWPLTQVTFYRDGSALGPPGP  
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS  
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ  
VWKQSPQLEIRVQGASSAAPTILNPAPQKSAAPGTAPPEEAPGPLPPPTPSSSEDPGFSSPL  
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

**Signal sequence:**

amino acids 1-17

**Leucine zipper pattern sequence:**

amino acids 12-33

**Protein kinase C phosphorylation site:**

amino acids 353-355

0997544-10160



## FIGURE 21

CCCACGCGTCCGCCCACGCGTCCGCCCACGGGTCCGCCCACGCGTCCGGGCCACCAGAAAGTT  
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG  
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT  
GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACCTATG  
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT  
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG  
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCCTGGAGATGG  
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG  
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC  
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC  
GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC  
AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA  
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG  
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
TTGAAAGCAACATCTACAGTGAAGCAGTCCTGGGACTGGACCACTGACATGGATGGCTACCT  
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT  
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGGAAGACATCCCAA  
CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCCATTTTTTGACCCCGT  
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC  
AATCCTAAGGCCGGAGGCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT  
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC  
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA  
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA  
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT  
CCAGTGATGAGCCAACTTCCCAGAATCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA  
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTCC  
TCTGGATTATGAGTTTCTGGCCACTGAGGGGCAAAGTGTCTGTAAAAATGCCCCATTAGGC  
CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCT  
ACCTCTCTTCTGGATAGCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT  
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG  
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG  
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA  
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT  
TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA  
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA  
ATCATAACAGC

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPTDYDPLQGYTQVLVKWLVQRGS  
DPVTIFLRDSSGDHIQQAKYQGRHLVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ  
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPISYIWYKQQTNNQE  
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTMT  
YPLKATSTVKQSWDWTDMGDLGETSAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKT  
SQQEHVYEAAR

### **Signal Sequence:**

amino acids 1-19

### **Glycosaminoglycan attachment site:**

amino acids 149-152

### **Transmembrane domain:**

amino acids 282-300

097544 10101  
TOSTOT 44582660

## FIGURE 23

GCGCCGGGAGCCCATCTGCCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCCGGCACAT  
GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCGCGCCAGCTCGCCCGAGGTCCGTCCGA  
GGCGCCCGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC  
GGGATGTCCTCCTCCTTCTCCTCTTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA  
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC  
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA  
GTGGTGATCACTTACTCCAGTCGTCTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGC  
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT  
GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT  
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT  
GACTACAACCACCTTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTA  
CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT  
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAAACCAGCT  
CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCTCCACTCGCTCCACAGCAAAT  
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC  
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG  
CTAATCTGACCAAAGCAGAAACCAACCCAGCATGATCCCAGCCAGAGCAGAGCCTTCCAA  
ACGGTCTGAATTACAATGGACTTGACTCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTC  
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
GTGAGCATTGCACGGAACAGATTGAGATGAGCATTTTTCTTATACAATACCAAACAAGCAAA  
AGGATGTAAGCTGATTCTCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG  
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTGGGGAAAGGTG  
AGGTGAATATACCTAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT  
TTCAAGAGGAAATGGGATGCTGTTTGTAATTTCTATGCATTTCTGCAAACCTATTGGATT  
ATTAGTTATTGAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
TGAGCTAACCCTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
TTCATTTGTGATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC  
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCATGATGTT  
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCCTCAAAT  
CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACAACATGTCATT  
TATCAACGTCTTAGAAAGAATTTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA  
CCCAACATACCATTTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAAATTGCAAGACTGG  
GTGGACTAGAAAGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLTMSSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 232-251

TOGETHER

## FIGURE 25

GTCGTTCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTTCGGAGGAGAGCACCCGGA  
GACGCGGGCTGCAGTCGCGGCGGGCTTCTCCCCGCTGGGCGGCTCGCCGCTGGGCAGGTGCTGAGCGCCCCCTAG  
AGCCTCCCTTTGCCGCTCCCTCCTCTGCCCCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG  
GCCCCGGAGGCGGCGGTGGATGCGGCGCTGGGCAGAAGCAGCCGCGGATTCCAGCTGCCCGCGCGCCCCGGGCG  
CCCCTGCGAGTCCCCGGTTTCAAGCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATC  
GCCCCCGGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCTTAGCACCACCACAGCTCAG  
CCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT  
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT  
GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG  
ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACCTTGCCACCTGGCATGTTCCAGTCTAACGCT  
ACCTGTGCCCCCATAACGGTGTGTCTGTGGGTTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG  
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCCTTCTAGTGTGATGAAATGCAAAGCATAACAGACTGT  
CTGAGTCAGAACCTGGTGGTGTATCAAGCCGGGGACCAAGGAGACAGACAACCTCTGTGGCACACTCCCGTCCCTT  
TCCAGCTCCACCTCACCTTCCCCTGGCACAGCCATCTTCCACGCCCCGAGCACATGGAAACCCATGAAGTCCCT  
TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACCTTCTGCTCTGTAGACCAAAGGTACTG  
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAAGGAAGACGTGAACAAGACCCCTC  
CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG  
GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG  
CATTTTGACATCAATGAGCATTTGCCCTGGATGATTGTGCTTTTCTGCTGCTGGTGCTTGTGGTGTGTTGGTG  
TGCAGTATCCGAAAAGCTCGAGGACTCTGAAAAGGGGCCCCCGGCAGGATCCAGTGCCATTGTGAAAAGGCA  
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCAGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT  
ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG  
AGGGAGGTTGCTGCTTTCTCAATGGGTACACAGCCGACCACGAGCGGGCTACGCAGCTCTGCAGCACTGGACC  
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG  
AAGATTCGTGGGCTGATGGAAGACACCACCCAGCTGGAAACTGACAACTAGCTCTCCCGATGAGCCCCAGCCCG  
CTTAGCCCCGAGCCCCATCCCCAGCCCCAACGCGAACTTGAGAATTCGGCTCTCCTGACGGTGGAGCCTTCCCCA  
CAGGACAAGAAACAAGGGCTTCTTCTGATGAGTGGAGCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC  
TCCGCGCTGAGCAGGAACGGTTCTTTATTACCAAGAAAAGAAAGGACACAGTGTGCGGCAGGTGACGCTGGAC  
CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTCTAAATCCTGAGGAGCTGCGGGTGTGTTGAAGAG  
ATTCCCAGGCTGAGGACAACTAGACCGGCTATTGCAATATTGAGTCAAGAGCCAGGAAGCCAGCCAGACC  
CTCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTAATCA  
ATTTAGTGGCAGGGTGGTTTTTAAATTTTCTTCTGTTTCTGATTTTGTGTTTGGGGTGTGTGTGTGTGTTGT  
GT  
TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTTATAAGCCTTTGCCAGGTGTAACCTGTTGTGAA  
ATACCCACCATAAAGTTTTTTAAGTTCATATTTTCTCCATTTTGCCCTTCTTATGTATTTTCAAGATTATTTCTG  
TGCACTTTAAATTTACTTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC  
TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT  
AAAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAAGAAATTTAAGA  
CCCCATTGAGTTACTGTAATGCAATTCACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTTATATTCATGG  
CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTACCTGGACACCGTGTAGAATGCTTGATTACTTGTAC  
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT  
GACAACTGGGCCACCAAAGAACTTGAACCTTCACTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT  
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCCAGCTTTGCTTTAAAGATGTCTTG  
TTTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCCTTGGTCTGTGGGATTCTTCCACCAATT  
ACTTTAATTTAAATGGCTGCACTGTAAGAACCTTGTCTGATATATTTGCAACTATGCTCCCATTTTACAAATG  
TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTGTGG  
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTTA  
AAAAA

CGCTTCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTTCGGAGGAGAGCACCCGGA

## FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPPSSSTALASCSRIARRATATMIAGSLLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG  
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFFTRHENGIEKCHDCSQPCPWPMIEKLPCA  
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKGTTETEDVRCKQCARGTFSDVPSSVMKC  
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSPFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP  
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL  
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVIVVCSIRK  
SSRTLKKGPRQDPSAIVEKAGLKKSMPTPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIY  
QFLCNASEREVAAFSNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRG  
LMEDTTQLETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL  
RCDSTSSGSSALSRRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ  
AEDKLDRLFEEIGVKSQEASQTLLDSVYSHLPDLL

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 350-370

109101-1453/660

## FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTGGGA  
 CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC  
CATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTGGCC  
 TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG  
 TCACTGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC  
 ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT  
 TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC  
 GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAAATGCCGTGCTCCAGGTGTTACAGCTGCTTC  
 GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCAAC  
 TGGGTTTTCCCAAGCTATGTGAGTTTCAATAACCTCAGAGTGAGCTCGCTGGAGGGGAGTTT  
 CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA  
 CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCACTGCACAGCCT  
 GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAG  
 TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGCTACCACCTGTGCGGGGGCTCTGTATCAC  
 GCCCCGTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA  
 CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG  
 ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT  
 GGCCGGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA  
 ACTTCCCCGATGGAAAAGTGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGAC  
 GCCTCCCCTGTCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG  
 GGACGTGTACGGTGGCATCATCTCCCCCTCATGCTCTGCGCGGGCTACCTGACGGGTGGCG  
 TGGACAGCTGCCAGGGGGACAGCGGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG  
 TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC  
 CCGTGTACCTCCTTCCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA  
 GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCT  
 GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCGGCACCA  
 GTAGCAGGCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTT  
 GTTTTTTGTTTTTTTTGGAGGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAA  
 TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCCTCAGCTTCCCCA  
 GTAGCTGGGACCACAGGTGCCCCGCCACCACACCCAACTAATTTTTGTATTTTTTAGTAGAGAC  
 AGGGTTTACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT  
 CAGCCTCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCAGCTCCTTTC  
 TGATCTTCACTAAGAACAAGAAAGAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT  
 CTGGTTTTTCTCTCCAGGGTCTTGCAAAATTCTGACGAGATAAGCAGTTATGTGACCTCACG  
 TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCAGAAGTGCAGAACTGCAGTC  
 ACTGCACGTTTTTCTCTAGGGACCAGAACCAACCCACCCTTTCTACTTCCAAGACTTAT  
 TTTACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT  
 TGTAGCATTTGGTGCTTGACGTATTATTGTCTTTGATTCCAATAATATGTTTCTTCCCT  
 CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

T09T0T"445E4660

## FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIILILA  
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLOVFTAAS  
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHH  
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGMNMSLLSQWPWQASLQFQGYHLCGGSVIT  
PLWIIITAAHCVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHISKYKPKRLGNDIALMKL  
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPLISNKICNHR  
DVYGGIISPSMLCAGYLTGGVDSCQGDGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYT  
RVTSFLDWIHEQMERDLKT

### **Signal Peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 240-284

109101-44582660



## FIGURE 29

CCCACGCGTCCGTCTAGTCCCCGGGCCAACTCGGACAGTTTGTCTATTTATTGCAACGGTCAAGGCTGGCTTGT  
GCCAGAACGGCGCGCGCGCGCACGCACACACGCGGGGGAACTTTTTTAAAAATGAAAGGCTAGAAGA  
GCTCAGCGGGCGCGCGGGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCCGGA  
CGCCCGGCCCCGGCTCGGCGCCCGGTGGGATGGTGACGCTCGCCGCGGGCCCGAGAGCTGCTGCACTGAAG  
GCCGGCGACGATGSCAGCGCGCCCGCTGCCCGTGTCCCCCGCCCGCCCTCTGCTCGCCCTGGCCGGTGTCT  
GCTCGGCCCTGCGAGGCCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTGAGTGCCTCTGT  
TCGAGTGGGGACCTCTGGATCCAGTGAAGAGCTTCGACTCCAGAATCATCCAGAAGTGTGAATATTGACT  
ACAACGGGAAAGCAAAGAACTGATCATAAATCTGGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTACGGAAAC  
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT  
ACGGGATATTCTGATTGAGCAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAAATGA  
AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAAACTCTTCCAGCGAAGAAGCTGAAAAGCGT  
CCGGGGATCATGTGGATCACATCACACACACCAACCTCGCTGCAAGAATGTGTTTCCACCACCTCTCAGAC  
ATGGGCAAGAAGGCATAAAAGAGAGACCCTCAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGCCAGACAACCG  
AGAGTTTCAGAGGCAAGGAAAAGATCTGAAAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCACGTTGACAA  
GTTTTACAGACCACTGAACATTGCGATCGTGTGGTAGGCGTGGAAGTGTGGAATGACATGGACAAATGCTCTGT  
AAGTCAGGACCCATTACACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTTTACCTCGCAAAATCCCA  
TGACAATGCGCAGCTTGTGAGTGGGTTTATTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG  
CACGGCAGACCAGTCTGGGGGAATTGTGATGGACCATTGAGACAATCCCTTGGTGCAGCCGTGACCCTGGCACA  
TGAGCTGGGCCACAATTTCCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA  
AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT  
GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTTAACTGCCGGAAGTCAGGGAGTCTTTCCGGGGCCA  
GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG  
CTGCAATGCCACCACCTGTACCCTGAAGCCGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT  
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGCCC  
TCACTGCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGSCAT  
CTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCCTGGGATCTGCTTTGA  
GAGAGTCAATTTCTCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCCCTTTGCCAAATGCCGAT  
GAGAGATGCTAAATGTGGAAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCAATTGGTACCAATGCCGTTTC  
CATAGAAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGGACCCACGTGTACTTTGGCGATGA  
CATGCCGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGAGATGGAAAAATCTGCCCTGAATCGTCAATGTCA  
AAATATTAAGTGTCTTTGGGGTTACAGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACCAACAGGAAGAA  
CTGCCACTGCGAGGGCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC  
CATCCGGCAAGCAGAAGCAAGGCAGGAAGTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG  
ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCAGTG  
CTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT  
TCCATGACAACAGACACAACACAGTTCTCGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA  
CAGTGCAAGGAAGGGCAGCGACTTCTGTTGAGCTTCTGCTAAAACATGGACATGCTTCAGTGTGCTCCTGAG  
AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC  
ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCAGTGTCCCCTTTCCCAGTGACACCTCAGCCT  
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAAT  
AGCAGGGTTTATGTTTAAATTTATCAGAGACCTGCCACCCATTCCATCTCCATCCAAGCAAACCTGAATGGCAA  
TGAAACAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC  
AGTACTCAGGTTTGGGGTTTGAGAGGCTTGCAGAAAGCCAGGGAACCCACAGAGTACCAACCCCTTCATTTAACAAGTAAGAA  
TGTTAAAAAGTGAAAAAATGTAAGAGCCTAACTCCATCCCCGTGGCCATTACTGCATAAAATAGAGTGCAATTT  
GAAAT

CGCTT" 44537660

## FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVVSASVRSGLWI PVKSFDSK  
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGH CYYHGHVRG  
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA  
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDKF  
YRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG  
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNF GMNHD TLD RGCSCQMAVEK  
GGCIMNASTGYPPFMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE  
CDCGEPEECMNRC CNATTCTLKPD AVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS  
PHCPANVYLHDGHSCQDVDGYCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN  
CGKVS KSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG  
DDMPDPGLVLAGTKCADGKICLNRQCQNI SVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP  
FCDKFGFGGSTD SGPIRQAEARQEAAESNRERGGQEPVGSQEHA STASLT LI

**Signal peptide:**

amino acids 1-28

09534453650

## **FIGURE 31**

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA  
ACAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA  
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT  
GGGCCCAGTGTCCTCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTATTATATGAAAATAGCAGGGTTTT  
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

0997544.10160  
T09T0T"4458/660

## FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA  
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCCGCTCGGCCTCCC  
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTTAAGAAGTTAAT  
GAAACCATAACCTTTTACATTTTAAATGACAGGAAAATGCTCACAATAATTGTTAACCCAAAA  
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA  
TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA  
CTTTTAACAAAAAATTTGCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG  
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTGAAATCTGCCT  
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTCTAAGCAACTTAAATGTTTTGTTCGA  
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC  
TTGAATATAAGACCCTACTTGCTATCTCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC  
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA  
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTTGTT  
CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCT  
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG  
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT  
AGAAGTTCAATGTGGCAAGGAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT  
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT  
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG  
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA  
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG  
ACAATCACTTGAACTCAGGAGGCAGAGGTGTCAGTGAGCTGAGATCGCGCTACTGCACTCTA  
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAGTGGCT  
CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA  
AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGG  
GATGGTGGCAGGCACCTGGAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA  
CTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG  
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 33**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL  
LHLYH

**Signal peptide:**

amino acids 15-27

009544 10560

GCCTCCGGCGAGAGCGCGCCAGCCCGCCCGCGCATGCCCGCGCGCCAGGACGCCTCTCTCCGCTGCTGGCCCCGGC  
CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGCGGCATGGCGCGCGCGGGCGCTGGGGCGCCCCGGGCCAGG  
AGGCGGCGCGCGCGCGCGCGGACGGGCCCCCGCGCGAGACGGCGAGGACGGACAGGACCCGCACAGCAAGCACC  
TGTTACACGGCCGACATGTTTACGACACGGGATCCAGAGCGCGCGCACTTCGTCATGTTCTTCGCGCCCTGGTGTG  
GACACTGCCAGCGGCTGCAGCCGCACTTGAATGACCTGGGAGACAAATAACAACAGCATGGAAGATGCCAAAGTCT  
ATGTGGCTAAAGTGGACTGCACGGCCCCACTCCGACCTGTGCTCCGCCCCAGGGGTGCGAGGATACCCCACTTAA  
AGCTTTTCAAGCAGGCCAAGAAAGCTGTGAAGCTACAGGTCCTCGGGACTTCAGACACTGGAAAACTGGATGC  
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAAGTGGAACCGCCAGTGCCTCCGAGCTCAAGCAAG  
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC  
CGTGGTGTGGTCACTGCAGAACCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCCGAAACTG  
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTGTCTCCGAAACAGGTTCTGCTGCTATCCCACT  
TTCTCTGGTTCCGAGATGGGAAAAAGTTGGATCAGTACAAGGAAAGCGGGATTTGGAGTCACTGAGGAGTACG  
TGGAGTCGCGAGCTGCAGCGCACAGAGACTGGAGCGACGAGACCGTACGCCCCCTCAGAGGCCCCGGTGTCTGGCAG  
CTGAGCCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAAATAACTTCGATGACACCATTGCAGAAGGAA  
TAACCTTCATCAAGTTTTATGCTCCATGGTGTGGTCATTGTAAAGACTCTGGCTCCTACTTGGGAGGAACCTCTCTA  
AAAAGGAATTTCCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACCTGCTGAACGGAATATCTGCAGCA  
AGTATTCGGTACGAGGCTACCCCACTGTTATTGCTTTTCCGAGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCA  
GAGACCTTGACTCGTTACACCGCTTTGTCTTGAGCCAAGCGAAAGCAGCACTTTAGGAAACAGATTGGAGGTAC  
CTCTCCTGGCCAGCTCCCCGCACCCCTGCGTTTAGGAGTTTCACTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT  
GTTTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTGTGTTTTCCAAGCCAACACACTCTACAG  
ATTCTTTATTAAGTTAAGTTTTCTCTAAGTAAATGTGTAACCTCATGGTCACTGTGTAAACATTTTTCAGTGGCGATA  
TATCCCCCTTTGACCTTCTCTTGATGAAATTTACATGGTTTCTTTGAGACTAAAATACGTTGAGGAAATGAAA  
TTGCTGGACTATTTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAACATCCAAAGCAGGTTTACCTGCG  
CCACGAGTTCTGAAAGAGGTGGCTTTGTGGCAGTATTGACGTTTCTCTGATCTTAAGGTACAGTTGACTCAATAC  
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCCTGGAAGATACCTTCACGGCCGCTGC  
TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC  
GTGCCTGAGTAAGAGAAATGCTGATGCCATAACTTTTATGTGTGATGATACTTGTCAAATCAGTTTACTGTTTCAGGGGAT  
CCTTCTGTTTCTCACGGGGTGAACACTGTCTTTAGTTCTCATGTTTAACCAAGCCAGAGCCACAGCTGAACTGT  
TGGATGCTTCTTCTTAGAAAGGTAGGCATGGAATAATCCACGAGGCTCATTCTCAGTATCTCATTAACTCATTTGA  
AAGATTCCAGTTGTATTTGTACCTGGGGTGACAAGACCAGACAGGCTTTCCAGGCCCTGGGTATCCAGGGAGGC  
TCTGCAGCCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCCTTTTAGAGG  
CTTGCTATACTTGGTCTGCTTCAAGGAGGTGACCTTCTAATGTATGAAGATGGGATGCATTTGATCTCAAGAC  
CAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA  
ACTCATGCTGTCTTGTGATTAAACACCTCTATCTCCTTGGGAAATAAGCACATACAGGCTTAAAGCTCTAAGATA  
GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCATAATAAACCACCTTGTGATCCAACACTCTTACCCACCT  
CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCACCTTATA  
CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCAG  
TATGGTTCAAGATAAATCTTTTTTAAAAAACCCCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA  
CACAACCTCAGCTTTGCATCAGAGTCTGTATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTTTACACTAT  
GACTTTTTCTAAATAAACTCTTTTTTTTTTAA

## FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS  
KHLYTADMFTTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH  
SDVCSAQGVRGYPTLKLFPKGQEA VKYQGPRDFQTLNWM LQTLNEEPVTPEPEVEPPSAPE  
LKQGLYELSASN FELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT  
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGRDLESLREYVESQLQRTETGATETVTPSEA  
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA  
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

**Signal sequence:**

amino acids 1-32

44582660

## FIGURE 36

CTTTTCTGAGGAACCACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT  
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA  
CCGCTGAAGTCTGTGCCACACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA  
GGAGATCCAGGAGAAGAGGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA  
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT  
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG  
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA  
TGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT  
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTTCCTG  
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT  
CCATCATCAAAAAAAAAAAAAAAAAA



## **FIGURE 37**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPGEEG  
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKKGAGTVCDGCRY  
RKFBVGQLDISIARLKTSMKFVKNVIAIRETEEFYIVQEEKNYRESLTHCRIRGGMLAMP  
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC  
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

**Signal peptide:**

amino acids 1-25

109101"4453/660

## FIGURE 38

GGTTCTATCGATTTCGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCTGCTCTCCGCCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT  
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT  
CGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC  
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA  
AGCTACACCTCTGGCCGCGAGTTGCGCTGGCTTCGGGCGGACTTGGCCTTTGCGGTGCGAGCT  
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG  
TCCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACTGGCCCAGCAGCGCGCCGCGC  
ACACCTTTCTCATTCACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC  
AGGGCTGCACGCGCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAG  
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG  
GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT  
CTGTCACTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCAGAGTTTCTGTGGCTCTG  
GTTCCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCC  
CCCTGCTGCACTGCCTCCGAGCTGCGGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG  
GAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG  
CCCAGGAACCCACCCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG  
GGCCAGTGCCAGGATACCTCTCTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC  
ACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG  
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCAC  
TCTACCACATGTCCGGTTCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG  
GTGCTGAAATCCAAGTTCTCGGCTGGTCACTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC  
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTTGTCAACCAGCCCCCGAGCAAGGCAG  
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT  
TTTGTGCGGCGCTTCGGGCCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT  
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGC  
ATATCTTCCCCCTTCTCCTTGATTGCTATGATGTCAACACAGGAGAGCCAATTCTGGGACCCC  
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA  
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCAGGGGAAGTTGCTAAAGG  
ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA  
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC  
CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG  
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC  
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG  
GCCCCGATTCTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG  
TTCGGATGGCAAATGAGGGCTTCGACCCAGCACCTGTCTGACCCACTGTACGTTCTGGAC  
CAGGCTGTAGGTGCCTACCTGCCCTCACAACCTGCCCGGTACAGCGCCCTCCTGGCAGGAAA  
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACCTCTGTGGGGTGGGG  
CCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT  
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC  
TTGGCCGCATGGCCCAACTTGTTTATTGCAG

## **FIGURE 39**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913

><subunit 1 of 1, 730 aa, 1 stop

><MW: 78644, pI: 7.65, NX(S/T): 2

MGVCQRTAPWKEKSQLERAAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLLPL  
LLLKLHLWPQLRWLPADLAFVRLCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ  
RAAHTFLIHGSRFSYSEAERESNRAARAFLRALGWDWGPDPGGDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA  
EVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP  
SKAERGHKVRILAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW  
LYKHIFPFSLIRYDVTTGEPIDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQGK  
LLKDVFRPGDVFFNTGDLVLCDDQGFLRFHRTGDTFRWKGENVATTEVAEVFEALDFLQEV  
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK  
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI

**Type II transmembrane domain:**

amino acids 45-65

**Other transmembrane domain:**

amino acids 379-398

**cAMP- and cGMP-dependent protein kinase phosphorylation site**  
starting at amino acid 136

**CUB domain protein motif**

amino acids 254-261

**putative AMP-binding domain signature**

amino acids 332-343

**N-glycosylation sites**

amino acids 37-40 and 483-486

## FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA  
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATAACACTCGCTCTC  
GCTTGTCCATCTCCCTCCCGGGGAGCCGGCGCGCTCCACCTTTGCCGCACACTCCGGC  
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC  
CCATGGTGGTTTTTTTAAACACTTCTTTTCCTTCTCTTCCCTCGTTTTTGATTGCACCGTTTTCCA  
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTTGGCTTGCCATCGT  
CCATCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGG  
CTGGCAGAAGGGGGTGACGCTGGGCAGCGGCGAGGAGCGCGCCGCTGCCTCTGGCGGGCTTT  
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTGTATG  
TTGCACCAATGCCTTCTTGATCGGGGCTGTGATTCTTCCCCTCTTGGGGCTGCTGCTCTCCC  
TCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCGCCAGGCGTACGGTGCC  
AAGGGATTTCAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG  
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC  
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG  
CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA  
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTGAGAAGTCTTCCAGGACCTCT  
TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC  
TTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCCCTCAGTATCACTTCAGTGA  
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC  
GGAACTGAAGATTTCAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG  
ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTGAGCCCAACCCAGGGTGTATCCG  
TGCCCTCATGAAGATGCTGTACTGCCCATACTGTGCGGGGCTTCCCACTGTGAGGCCCTGCA  
ACAACTACTGTCTCAACGTATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG  
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT  
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA  
ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCC  
CTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTTCAGGCCCTACAATCCTGA  
GGAAAGACCAACAACTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA  
AATTGAAGCTCTCTAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC  
GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT  
GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA  
TCACTCGGCCTGACACTTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA  
CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG  
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCCACGGAGTTTGAGTTTGTACCA  
CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC  
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTTGGCACTGCAGAGACTGTGCAGATTA  
ATCTTGGGTTTTTTGGTCAGATGAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTT  
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACTTACCGTTTTCTATGAGAAGAGAG  
CAGTAATGCAATCTGCCTCCCTTTTTGTTTTCCCAAAGAGTACCGGTGCCAGACTGAACTG  
CTTCCCTCTTTCCTTTCAGCTATCTGTGGGGACCTTGTTTATTCTAGAGAGAATTCTTACTCAA  
ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAAT  
CTCACGTTGTGAGGGTTTTTTTTTTCTCATTAAAT

## **FIGURE 41**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKARSCGEVRQAYGAKGFSLADIPYQEIAGEHLRICPQ  
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF  
VRTYGMLYMQNSEVFQDLFTTELKRYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY  
LECVSKYTDQLKPFQDVPRKLIKQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL  
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES  
VMDPIDVKISEAIMNMQENSMQVSAKVFQGCQPKPAPALRSARSAPENFNTRFRPYNPEER  
PTTAAGTSLDRLVTDIKEKLKLSKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE  
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG  
SGSGCMDDVCPTFEFEVTTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

**Signal peptide:**

amino acids 1-23

0974453660

## FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG  
CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACCTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG  
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT  
GGAGGGAGATCAGGAAACGGCTTCTTCCTCACTTCGCCGCTGGTGAGTGTGCGGGAGATTGGCAAACGCCTAGG  
AAAGGACTGGGGAAAATAGCCCTGGGAAAGTGAGAAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG  
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA  
TCCCGCCGCCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCCAACGTGAGGGCGCTCTGGCCACGA  
AAAGTTCTGTCCACTGTGATTCTCAATTCCTTGCTTGGTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA  
ACTTTTTTCTTTTTTTTTTTTCTTGGTGGAAGCTGCTCTAGGGAGGGGGGAGGAGGAGAGAAAGTGAAATGTGC  
TGGAGAAGAGCGAGCCCTCCTTGTCTTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT  
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTCACCGTCTGTTGGGTGCATG  
TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA  
GGGGCTGTGCGGGGCATCCGCCTCCGCCTTCTCCACAGGCCTGTGTCTGTCTCTGGAAGATGCTAGCAATGGGGG  
CGCTGGCAGGATTCCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTCTGGGGCCAGGCCTTAGAAGAGGAGG  
AAGAAGGGGGCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCCAGCACAACTTCCACCTCCAGCCCCATCTCA  
TTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTACCACGGATCTGAGATTAAAACACCTACTCTTG  
ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT  
TTATTACTGGAAAGTATCAGATACACACCGGACTTCAACATTTCTATCATAAGACCTACCCAACCCAACCTGTTTAC  
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTTCGGAAAATGGCACT  
TGGGTTTTTAACAGAAAAGAATGCATGCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG  
GGGATTACTATACACACTACAAATGTGACAGTCTTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG  
CCTGGGACTATGACAATGGCATATACCTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCATA  
ACCCACAAAGCCTATATTTTTATATACTGCCTATCAAGCTGTTCACTTCACTGCAAGCTCCTGGCAGGTATT  
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCTGCTTAGATGAAGCAA  
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG  
GTGGCCAGCCTACGGCAGGAGGGAGTAACTGGCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC  
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACTTGTGCACATCACTG  
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT  
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCGAGTAGATATTTTGCATAACATTGACCCCTATACACCAAGGC  
AAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG  
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG  
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA  
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAAC  
TGCAGTGCCGCTCAGGTATCCCCCAGAACCCAGAAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG  
GTATAAAGAGGAAACCAAGAAAAAGAAAGCAAGCAAAAATCAGGCTGAGAAAAAGCAAAAGAAAAGCAAAAAA  
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA  
GGCTTGTTTTTATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCCACTGAAAACCTGTCTGTCTCAGTG  
CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTTATTTCTCTCGCTCCTTTAGAAAACGTG  
GTGAGTCTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAAACACTGCTTTGAATTATAGGAGGAGAACATA  
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAAACTACCTTTGATAAATTAC

## FIGURE 42B

AGTCAAAGATTGTGTACCTCAAAGGCCTTGAAGAATATATTTTCTTGGTGAATTTTGTATGTCTGTTCATATGA  
CACTTGGGTTTTTTAATTAATTCTATTTTATATATATAAATATATGTTTCTTTTCCTGTGAAAAGCTGTTTTTCT  
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC  
ACAATGAATGTAACATATTTTCTAAACACTTTACTAGAAGAACATTTTCAGTATAAAAAACCTAATTTATTTTACA  
GAAAAATATTTTGTGTGTTTTTATAAAAAGTTATGCAAATGACTTTTATTTTATTTTCCTGCATACCATTAGAAGA  
ATTTTATTTTCATTTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA  
TAAAAACATCATTCAGAAAACCTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT  
ATTACTTGGAAATTCATGTTTGTGTCAGAGTTGAGACAACTTTATTGTTTCTATCATAAACTATTTATGTATCTT  
AATTATTTAAATGATTTACTTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAAGTTCTAGCTAAAAAT  
GTATCATTTGGTCTTAAAAAATAAAAACTTTTACTAATAGGCAATTGAAGGAATGGTTTGTCTAACAACCACAGTAA  
TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAGATTTTCCCATATAATAACTAA  
TATTTATATTAGGTTGGTGCAAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT  
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGGAAACCCC  
ACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA  
GATTGGTGTGGATCCTGTAGACCTGGTGTTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTTGAAGCTTAC  
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT  
GGTGGTATGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC  
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAATCTATAAT  
CTAGTACTGAAATTACTAAATTGGGTAAGATGATTTAAATGATTTTAAATTTTAAACATTTTATTTCTAGAATATAT  
GGCTCCATTTTATTTTATAGTGTAAGTTGTATTTCTTAAAGTTTGTGTTTTGTGCGACAGTATCTTTTAAATGAG  
TC'TTAAAAATAAAGGCATATTGTTTCATGTTTAAA  
AAA

## **FIGURE 43**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEGALLAQA  
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAAGVKLENYYVQPICTP  
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGKWHLGFNKKEC  
MPTRRGFDTFFGSLLGSGDYIYTHYKCDSPGMCYDLYENDNAAWDYDNGIYSTQMYTQRVQQ  
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA  
LKTYGFYNNSSIIIIYSSDNGGQPTAGGSNWPLRSGSKGTYWEGGIRAVGFVHSPLLKNKGTVC  
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG  
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS  
TSQPTHMRGWTYLTGIQES

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-37

#### **Sulfatases signature 1.**

amino acids 120-132

#### **Sulfatases signature 2.**

amino acids 168-177

#### **Tyrosine kinase phosphorylation site.**

amino acids 163-169

#### **N-glycosylation sites.**

amino acids 157-160, 306-309 and 318-321

099544-44582660



## FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC  
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC  
CCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG  
GTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCT  
GGGGTCTGTCACTATGGAACATAAAGTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG  
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAAACAAAT  
GCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG  
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT  
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACTCTAGGACATGTGCCATGATAA  
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA  
CTCCGCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT  
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACA  
TTGGTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT  
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCTTTCAAGTG  
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG  
TGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC  
AAAAACAGCATGAAAAAGAAGGCAAAAATTAAAAATGTTACCCCAAGAACCCACCAGGACTCC  
TACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAC  
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAAGAGGGGCTTGAGGATGAGAAAAGAG  
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCCT  
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAAGTTCCAA  
ACTGGAACATAAAGATTTAAATATCTCGTTGACTGCAGCTTCAATCATGGGATCTGTGACT  
GGAAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC  
TTCTATATGGCAGTTCCGGCCTTGGCAGGTACAAGAAAGACATTGGCCGATTGAAACTTCT  
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG  
ACAAAGTCGGGAAACTTCGAGTGTGTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG  
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAATTGAGTTGTATCAAGGAAGTGTATGC  
TACCAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCGAAATCGCAGTGG  
ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG  
TTACTATCTTTATATTTGACTTTGTATGTGAGTTCCCTGGTTTTTTTGTATATTGCATCATAG  
GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG  
TAAGATGCCTTTCTTGATATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT  
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC  
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA  
GAAAATAGAAAAAAAAGCACAGAGAAATGTTTAACTGTTTGAAGTCTTATGATACTTCTTGGA  
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC  
TTGTATATTTAATTCCTTTGTAATAATAA

## **FIGURE 45**

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNRNSKGVCE  
ATCEPGCKFGECEVGPNNKCRCPGYTGKTCSDVNECGMKPRPCQHRCVNTHGSKCFCLSGH  
MLMPDATCVNSRTCAMINCOYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP  
YNNRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK  
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPPK  
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

### **Signal peptide:**

amino acids 1-21

### **EGF-like domain cysteine pattern signature.**

amino acids 80-91

### **Calcium-binding EGF-like domains**

amino acids 103-124, 230-251 and 185-206

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## FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG  
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC  
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG  
AGCTGGCTTACCAGTTGTCTAACTAGGAGTTTCTCTTGTGCTGTCAGCCAGAAGAGTGCAT  
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT  
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGAATGTCCCAGCGTTCTCTGTGC  
ATGGATAACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC  
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCATTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATAACCAGGTATAATAGTTTC  
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG  
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT  
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC  
TTTAAGACAAAACATGA<sup>CT</sup>GAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT  
ACTTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAATAATAAAAG  
ATTGCCATGAATCTTGCAAAA

## **FIGURE 47**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343

><subunit 1 of 1, 289 aa, 1 stop

><MW: 32268, pI: 9.21, NX(S/T): 0

MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL  
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRS LCMDTSLDVYRKLIELNYLGTVSLTKCVL  
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP  
VQSNIVENSLAGEVT KTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW  
QYMPTWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 136-157

#### **Tyrosine kinase phosphorylation site.**

106-113 and 107-114

#### **Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

099744582660

## FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTGCGCGCTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCGG  
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC  
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTC  
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT  
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA  
ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG  
GACAGCGTGGCCCCGGCCCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC  
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC  
CTGGGTCTCTACTGCTGCCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT  
CAGTGGTCTTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG  
GCTGCCCTGCAGTTGCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC  
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC  
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGTATCTACAACAGCT  
GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGGCCCCCAGCCTG  
GGGTGCAGGGCCCCCTGTGAGGAGATTCCGGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA  
CACTGGGTTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT  
GCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTT  
TCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA  
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCT  
GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTG  
CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA  
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG  
CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC  
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG  
GCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG  
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG  
TGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCACCACCTGGTG  
CATGAGGTGAGGGGCACATGGTTCTTGCCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG  
CCCCGCCAGGCCGGCGGTCTTACCCGCGCTCCCTGCCCTATGAGGACTGGGTGAGCAGTTTGG  
ACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCCAGGCTGAGCCTGGAAGCTGCCTGGCC  
AACATAAGCCAACCAACCAGCTGCTGAAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC  
AGGCAGGCAAATGGCATTACTGCCCTGTCTCCTCCCCACCCTGTCATGTGTGATTCCAGGCAC  
CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA  
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC  
AGGCGTCTCAGCTTTCCTCCTCTTACTCTTTCAGATACAATCACGCCAGCCACGTTGTTT  
TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCCTTTTTTTTAACTTAAATAAATTGTTAC  
AAAATAAAA

## **FIGURE 49**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQ GKAKRHGNTV  
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGA  
EEVGVAALQLPRAYNHYSQGS DLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS  
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC  
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS  
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV  
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHL PDGERG  
WVLGRARPGAGISSLQTVPVTL LGPRACSR LHAAPGGDGS PILPGMVCTSAVGELPSCEGLS  
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAE P  
GSLANISQPTSC

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

#### **N-glycosylation sites.**

amino acids 37-40 and 564-567

#### **Kringle domains**

amino acids 79-96, 343-360 and 235-247

## FIGURE 50

CGGGCCGCCCCCGGCCCCCATTCGGGCGGGGCTCGCTGCGGCGGCGACTGAGCCAGGCTGG  
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAG  
CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT  
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG  
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC  
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATAACCAACA  
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC  
TCTTCCCGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGGGTGTGGCG  
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCCGGCAGCGCTGCCGTGAGCCT  
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC  
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTT  
TGGCAGGATGGGCAGGGTGTGCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA  
GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGTGCTGGGTGCGAATGGCACCTACA  
GCTGCCTGGTGGCAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCACCATCACAGGG  
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT  
TGCACTGCTGGTGGCCCTGGCTTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG  
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT  
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG  
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC  
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC  
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT  
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT  
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC  
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA  
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTC  
TCCAATGGCCGTGATACACTAGTGATCATGTTTCCAGCCCTGCTTCCACCTGCATAGAATCTTT  
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTC  
CCCTCCTTCTCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG  
AGGGGACTGCCCCCACCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCCTGGC  
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG  
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC  
TCGGAGGGATTTTGTAACCTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA  
AAAAAAAAAAAAA

## **FIGURE 51**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ  
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV  
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGVPL  
TGNVTTSQMANEQGLFDVHVSRLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA  
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEEENAGAEDQDGEGEGSKTALQPLKHSDSKED  
DGQEIA

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 251-270

#### **N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

#### **Homologous region to Immunoglobulins and MHC**

amino acids 217-234

TOGETHER: 44584660



## FIGURE 52

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC  
CTGAACTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG  
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCTTGCTTCAGCAACATGAGGCTTTTCT  
TGTGGAACGCGGTCTTGA CTCTGTTCTGTCACCTTCTTTGATTGGGGCTTTGATCCCTGAACCA  
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCTCTGCCATCGCAAGACCAAAGGAGGGGA  
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC  
ACAAACATAACAATGGTCAGCCCATTGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT  
TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGC  
TCTGGGCTATGGAAAAGAAGGAAAAGGTAAAATTCCCCCAGAAAGTACACTGATATTTAATA  
TTGATCTCCTGGAGATTGCAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT  
AATGATGACTGGAACTCTCTAAAGATGAGGTAAAGCATATTTAAAGAAGGAGTTTGAAAA  
ACATGGTGC GGTTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTTGATAAAG  
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA  
TAGAGATACATCTACCCTTTTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA  
AGAACATTTTATTTTTTATACAATGTTCTTTCTTGCTTTGTTTTTTATTTTTTATATATTTTTT  
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT  
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTCACAG  
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAAATGTTGCAACTGGGAATATACC  
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCATATTTCTGCTTCCCTCTATTTTCT  
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTTCAT  
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA  
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG  
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG  
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA  
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCT  
ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG  
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA  
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT  
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG  
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC  
TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA  
TTGTATCATAAGATAAAGTAGTAAACCACTACATTTTCCCATTTCTGTCTCATCAAAAAC  
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGG  
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA  
CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGACACCTGTAGTCCCAGCTACTCGGGAG  
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC  
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA  
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

## **FIGURE 53**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194

><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGS  
L  
FHSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST  
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED  
IFDKEDDKDGFISAREFTYKHDEL

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 176-179

**Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

**Endoplasmic reticulum targeting sequence.**

amino acids 208-211

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

**EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

**S-100/ICaBP type calcium binding domain**

amino acids 183-203

## FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT  
CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCCTAGCCCACCCGA  
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT  
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC  
CTGCCACCCTCAACGTCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGC  
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC  
TGAGGAGATGTTCTCCAGTTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTTCAAG  
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTG  
CAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGG  
CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG  
CCGTGATTGTGGGTGCCCTCCGTGGGGGGCTTCTGGCTGTGGTCATCTTGGTGCTGATGGTG  
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA  
GGAGGGCAAGACGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC  
CTGCAGCCTCCCCTGTCCCCTCTCTCCCCTCTCCGCCCTGTACAGTGACCCTGCCTGCTCG  
CTCTTGGTGTGCTTCCCCTGACCTAGGACCCAGGGCCACCTGGGGCCTCCTGAACCCCCG  
ACTTCGTATCTCCCACCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA  
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGG  
GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA  
GGAGGGGCCGCTGTACCTGCCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTG  
GGAGGGAGGGCTTCTCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG  
TGCTCCTCCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTGA  
AACTTGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG  
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTTCCATT  
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG  
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCC  
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTGCTGCAG  
GCTCTGCCTTCTCCATGGGGTAACCACCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT  
GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCTTTGGGGCTTCAGTGAGAACTCTCCCAGTT  
GCCCTTGGTGGGGTTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCG  
GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG  
CTACTCGCTCCTCTCCCAACAACTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC  
ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT  
CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG  
GTGGCGTGTGCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG  
GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC  
ATAGAGAGACTCCATCTCAAAAAAA

CGTCTT"44582660

## **FIGURE 55**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNLNGSDARLPCTFNSCYTVNHKQ  
FSLNWTYQECNNCSEEMFLQFRMKIINLKLRFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI  
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK  
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 161-179

**Immunoglobulin-like fold:**

amino acids 83-127

**N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

FIGURE 55

## **FIGURE 56**

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCACCCNACTAACATCTCAGTCTCTGAA  
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT  
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC  
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC  
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG  
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCAGCAAGTACGATGTGTGCGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA  
TTTACAACCTGCTACATCATGAACCCCC

FIGURE 56

## **FIGURE 57**

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCCAACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCCTCAACGTCCTCAATGGCTTTGACGCCCCGCCTGCCCTGCACCTTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC  
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG  
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCCAGCAAGTACGATGTGTCGGTGATGC  
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCC

099707 44532660

## FIGURE 58

TGCGGCGACCGTCTGTACACCATGGGCCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCCTCCTGT  
TCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGGACGTCAACCCCAAGTGGTGTGCTGGTCC  
CTGGTGATTTGGGTAAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGA  
CCGAAAGCTACTTCACAATCTGGCTGAACCTGGAACTGCTGCTGCTGCTCATCATTTGACTGCTGGATTGACAATA  
TCAGGCTGGTTTACAACAAAACATCCAGGGCCACCCAGTTTCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG  
GGAAGACCTTCTCACTGGAGTTCTGGACCCAGCAAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGA  
GCCTTGTGGGCTGGGGCTACACACGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG  
AAAACGGGCCCCCTACTTCTGGCCCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTGGTGC  
TGTTTGCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGAGGCCTGGAAGGACAAGT  
ATATCCGGGCCCTTCGTGTCACTGGGTGCGCCTTGGGGGGGGCGTGGCCAAGACCCTGCGCGTCTGGCTTCAGGAG  
ACAACAACCGGATCCCAGTCACTCGGGCCCCCTGAAGATCCGGGAGCAGCAGCGGTGAGTGTCTCCACAGCTGGC  
TGCTGCCCTACAACATACATGGTCACTGAGAAGGTGTTCTGTCAGACACCCACAATCAACTACACACTGCGGG  
ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG  
AAGCCACGATGCCACCTGGCGTGCAGCTGCCTCTATGGTACTGGCGTCCCCACACAGACTCCTTCTACT  
ATGAGAGCTTCCCTGACCGTGACCCATAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACCTGAAGAGTGGCC  
TGATGCTCCAGGCTGGCAGAGCCGCCAGGAGCACAAGTGTGCTGTCAGGAGCTGCCAGGCAGCGAGCACATCG  
AGATGCTGGCCAACGCCACCACCCTGGCCTATCTGAAACGTGTGCTCCTTGGGCCCCTGACTCCTGTGCCACAGGA  
CTCCTGTGGCTCGGCGCTGGACCTGCTGTTGGCCTCTGGGGCTGTGATGGCCCACGCTTTTGCAAAGTTTGTGA  
CTCACCATTCAAGGCCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTTGTATCCTTTCTCT  
GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGA  
ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCCCTGGTCCCAGTCCCTGCCTGGGGCCATG  
TGTCCCCCTATTCTGTGGGCTTTTCATACTTGCCTACTGGGCCCCCTGGCCCCGAGCCTTCTATGAGGGATGTT  
ACTGGGCTGTGGTCTGTACCCAGAGGTCCAGGGATCGGCTCCTGGCCCCCTCGGGTGACCTTCCCACACACCA  
GCCACAGATAGGCCTGCCACTGGTCACTGGGTAGCTAGAGCTGTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC  
TGACTGGCTTCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGCGAGTTGTGTGCGTTCTTCGTGGTTCCCAGGC  
CCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCATTCAGCTCTGGATTGGGCAGCAGATGTG  
CCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCCGATTTCCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC  
CTCCCTTCAACCTGGGACTGTGGTTCCAAGGATGAGAGCAGGGGTGGAGCCATGGCCTTCTGGGAACCTATGGA  
GAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCACCATCA  
CACTGCCACCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTGAGCACAGGGCTGAGGATGGGGCTCCTATCCAC  
CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCCAGAACTTGAATGGGACCTGAGAGAGCCAGGGGTCCCC  
TGAGGCCCCCTAGGGGCTTTCTGTCTGCCCCAGGGTGTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT  
CAGGGCTGCCTTCATGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGT  
GGGGTTCCCAAAGACGCTTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGACAGCTGGATTCTCTCTG  
TTGCATACATGCCTGGCATCTGTCTCCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG  
GATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAA

TCGTCT"44582660

## **FIGURE 59**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH  
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVVPFGKTFSL  
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEEMYQ  
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI  
PVIGPLKIREQQRSVSTSWLLPYNYTWSPEKV FVQTPTINYTLRDYRKFFQDIGFEDGWLM  
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ  
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Potential lipid substrate binding site:**

amino acids 147-164

#### **N-glycosylation sites.**

amino acids 99-102, 273-276, 289-292 and 398-401

#### **Lipases, serine proteins**

amino acids 189-201

#### **Beta-transducin family Trp-Asp repeat**

amino acids 353-365

109101: 44582660



## FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGG  
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA  
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG  
AGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT  
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT  
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG  
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGGTTGGTTTCTGCTTCCTCACCAAC  
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT  
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCCTTCACCCAGAA  
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA  
GGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAAC TGCCA  
GCCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA  
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGGCCCCGGTTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG  
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCTCA  
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT  
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG  
CTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC  
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC  
TGTGCCGAGTGATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG  
GAATAAATGTTTTCTCATTCAAAG

09973544.101601

## **FIGURE 61**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAGAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYGSNAHESKQMYCVFN  
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLFIGDLLFSALWTFLWFGFC  
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP  
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPVY

### **Important features:**

#### **Type II Transmembrane domain:**

amino acids 1-45

#### **Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

#### **N-glycosylation site.**

amino acids 97-100

14582660

## FIGURE 62

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG  
CCCGTGGCCGAGGCCCCCGAGGTGGCTGGCGGGCAGGGGGACGGAGGTGATGGCGAGGAAGCGGAGCCAGAGGGG  
ATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCCCGGGGTACCTCCGCCTGGTGCCCTGTTTGTGCTGCTG  
GCCCTGCTCGTGCTGGCTTCGGCGGGGGTGCTACTCTGGTATTTCTAGGGTACAAGGCGGAGGTGATGGTCAGC  
CAGGTGTACTCAGGCAGTCTGCGTGTACTCAATCGCCACTTCTCCAGGATCTTACCCGCCGGAATCTAGTGCC  
TTCCGCAGTGAAACCGCCAAAGCCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCGCCCTGGGAACCTTACTAC  
AACTCCAGCTCCGTCTATTCTTTGGGGAGGGACCCCTCACCTGC'TTCTTCTGGTTCATTCTCCAAATCCCCGAG  
CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGCAGGCACTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC  
TCGGCTGCCGTCCCCTACAGGGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAA  
GACATAGCTGCATTGAATTCACGCTGGGTTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCTCCGGCTG  
AAGGGGCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGACCTCATGCTCAAACCTCCGG  
CTGGAGTGGACGCTGGCAGAGTGCCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCCCTGGAGAAGAGGCTC  
ATCACCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGTCCGGGGCCATCATGGCGGTC  
GTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCTGT  
GAAGTGAACCTGACGCTGGACAAAGGCTCGACTCCCAGGGCGTCTCAGCACCCGTACTTCCCAGCTACTAC  
TCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGATGCC  
TATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT  
GGCTTGCGCATCCTGCAGCCCTACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACC  
TCCCAGATCTCCCTCACCGGCCCGGTGTGCGGGTGCACTATGGCTTGTAACACAGTCCGACCCCTGCCCCGGA  
GAGTTCCCTCTGTTCTGTGAATGGAATCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCCAACGGCCTGGAT  
GAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAGAGGACAGCACATGCATCTCACTGCCCAAGGTGTGT  
GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACC  
TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGCCCGACTGCAGGGACGGC  
TCGGATGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGATTTGTTGGTGGAGCTGTGTCTCCGAG  
GGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGGTGCACACATCTGTGGGGGGGCCCTCATCGCTGACCGC  
TGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCTCCACGGTGTGTGGACCGTGTCTCTGGGC  
AAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGGTGTCTTCAAGGTGAGCCGCTGTCTCTGCACCCGTACAC  
GAAGAGGACAGCCATGACTACGACGTGGCGCTGTGTCAGCTCGACCACCCGCTGGTGGCTCGGCTCGGCCCGCTGCGC  
CCCGTCTGCTGCCCGCGCTCCCACTTCTTTCGAGCCCGCCTGCACTGCTGGATTACGGGCTGGGGCGCCTTG  
CGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTGATCCACAGGACCTGTGCAGCGAG  
GCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCGGGTACCGCAAGGGCAAGAAGGATGCCGTGTAGGGT  
GACTCAGGTGGTCCGCTGGTGTGCAAGGCACTCAGTGGCCGCTGGTTCTTGGCGGGCTGGTCAGCTGGGGCCTG  
GGCTGTGGCCGGCCTAACTACTTTCGGCGTCTACCCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTG  
ACCTGAGGAAGTGCCTCCCTGCAAAGCAGGGCCCCACCTCCTGGACTCAGAGAGCCCAGGGCAACTGCCAAGCAGG  
GGGACAAGTATTCTGGCGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTGTCTCGTCC  
CTGATGTCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCCGAGGACC  
CAGGCCACACCCAGCCCTTCTGCCTCCCAATTCTCTCTCCTCCGTCCCCCTTCTCCACTGCTGCCCTAATGCAAG  
GCAGTGGCTCAGCAGCAAGAATGCTGGTTCTACATCCCAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG  
CTGTTTGGGCAGCCTTGCCCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCTGGTCTAACTTGGGATCTGGGAAT  
GGAAGGTGCTCCCATCGAGGGGACCTCAGAGCCCTGGAGACTGCCAGGTGGGCCTGCTGCCACTGTAAGCCAA  
AAGGTGGGGAAGTCTGACTCCAGGGTCTTGGCCCCACCCCTGCCTGCCACCTGGGCCCCACAGCCCAGACCCCT  
CACTGGGAGGTGAGCTCAGCTGCCCTTTGGAATAAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAAA

CCGTTTCTGCTGCTG

## FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152

><subunit 1 of 1, 802 aa, 1 stop

><MW: 88846, pI: 6.41, NX(S/T): 7

MPVAEAPQVAGGQGDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL  
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT  
YINSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY  
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLRLKGPDLHLASSCLWHLQGPDLML  
KLRLEWTLAECRDLAMVDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY  
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSSTPYFPSYSPQTHCSWHLTVPSLDYGLAL  
WFDAYALRRQKYDLPTQGWITIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP  
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS  
LPKVCDCGQPDCLNGSDEEQCQEGVPCGTFTTFQCEDRSCVKKPNPQCDGRPDGRDGSDEEHCD  
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIAADRWVITAACHCFQEDSMASVTL  
WTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA  
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG  
KKDACQGDSSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT

### Important features:

#### Type II transmembrane domain:

amino acids 46-67

#### Serine proteases, trypsin family, histidine active site.

amino acids 604-609

#### N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512

#### Kringle domains.

amino acids 746-758 and 592-609

#### Homologous region to Kallikrein Light Chain:

amino acids 568-779

#### Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

**THE**

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTTGCGCATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT  
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC  
CTGGAGAGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGAGAGCCACATTCCAGTGCAAAGAGGA  
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG  
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT  
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCTGGGGTGCACACATCTGTGGG  
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT  
GGCCTCCACGGTGCTGTGGACCGTGTTCCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG  
GAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT  
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTCGGCCGCCGTGCGCCC  
CGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCT  
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG  
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC  
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGTGACTCAGGTGGTCCGCTGGTGTGCA  
AGGCACTCAGTGGCCGCTGGTTCCCTGGCGGGGCTGGTCAGCTGGGGCTGGGCTGTGGCCGG  
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT  
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCCACTCCTGGACTCAGAGAGCCAGGGC  
AACTGCCAAGCAGGGGGACAAGTAT

## FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG  
CTCCGTGCCGCCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCCTGGCCG  
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTTGTTTTTTAAA  
ACTTCTGTTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCTCTGCTCTG  
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC  
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG  
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTGCGCCACAG  
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTACGGAT  
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAACTCGTGTGAGCCCTGCACACAAGA  
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA  
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG  
AGAAGGACGATTTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG  
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC  
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGACGATGCAGATTTTG  
TGGATGTCCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTCAGATGCCTGTG  
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT  
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG  
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTTGCCTTCCAGTGCAC  
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT  
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG  
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA  
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA  
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT  
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

109707-14582660

## FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRITSKDPEHE  
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL  
PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV  
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF  
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS  
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:**

**Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

TOGETHER

## FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCCCCTCCCCCGC  
TTCCCTGTGCGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT  
CGGCCAAAGTTTGGGCCGAAGAGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACCAGGCCAGACCAAGGGCGCTCG  
CTGCCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG  
AGAAGAGTGCGGCGGCGGACGGAGAAAACAACCTCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG  
CCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG  
CACCAGGGAGCCTGGGCGCCCCGGGGCTCCGCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTTCCG  
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG  
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCCAGCAGTGCTCTTAGAAGTGCAGGGCACCTTACAGA  
GGCCCCCTGGTCCGGGACAGCCGCACCTCCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG  
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCTACGCTCCCCCTCTCCAGCCAC  
TGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCCCGGGGCAACGTCAACCATCACTTACAGCTATG  
CTGGGGCCAGAGCACCCATGGGCGAGGGCTTCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCGTGAGGAAG  
AGTTTCACTGCGCTGAACACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCCTGTGGCGATGGCT  
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCTCCCTGCCCTTGCATG  
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCCACCCCCAGT  
CCTGCCATTTGGCTGCTGGACCCCCATGATGGCCGGCGGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGCTTTG  
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCACCTTCA  
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTTACCACACAGTTGCTTGGAGCA  
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCCTGTGGCTTAGGCT  
CTGGCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT  
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGCTGGCACCT  
CTGGTGCCACAGCCTGCTACCTGCCTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA  
GACGCTGTGCGCATTTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCCTGTATGAGACGTGGGTGTGCG  
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCGCAAGGTCATTACAG  
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA  
TTTCGCACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC  
CTTCTTACGGGCAGCTCATTTGCCAGGGTGCCATCCCACTGTAGAAGACTTTCTTACAGAGAATCCTAATGATA  
ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCCAGGTG  
CCCGCCGTGCTCAGCGGGGCGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGTGGGGCTTGCTCCCTCGAA  
CCAACACCCCGCTCGGGCCTCTGAGGCCAGATCCCAGGTACACCTTCTGCTGCTCCCTTGGAGGCCCTAGATG  
GTGGCACAGGTCCAGCCCGTGGAGGGCGGGCAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCACTGCCCCATCA  
AGGCTCCCTCCCATCTGCTAGCACGTCTCCAGCCCCACTACTGTCCCTGAAGCCCAGGGCCACTGCCCTCAC  
TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCTGTTGCCAGCCTGGGGCCCC  
CAGGACCAACCCGAGCCCCCTGGACCCCAACAGCAGTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG  
TGCCACTGGCTGAGCCGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG  
CTCTACTGAGGCCTCTCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCTCC  
ACCCTTCTCTCCCTGTCCCTGGATTTAGGGACTTGGTGGGCCTCCCGTTGACCCCTATGTAGCTGCTATAAAGT  
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT  
TCACCACCACCTGCTCCCCACGCCACCACCATTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA  
GGTCTGGACACTCCATCCTTGCCAAACCTTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAACCTAGAGA  
CCCTCCAGCCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG  
CTCACAAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAAATAAA  
GGAATCATACATCTC



## **FIGURE 68**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHPDRIIFPNHACEDPPAVLLEVQGTQLQRPLVRDSRTSPANCTWLIL  
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP  
MGQGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRCDGVDACGDGSDEAGCSSDPFPGLTPRP  
VPSLPCNVTLEDFYGVFSSPGYTHLASVSHPOQSWLLDPHDGRRLAVRFTALDLGFGLDAVH  
VYDGPGPPESSRLRLSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGNATYHVRGYCLP  
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT  
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPD CADGSDEWDCS  
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY  
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGRRLMRRLVR  
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA  
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGPPGPTRSPPGPHTAV  
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

## **FIGURE 69**

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG  
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA  
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC  
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATA  
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATAT  
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG  
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCAC TTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA  
GCCTGTGCATGAAAAAAAAGAAGTTTTGTAATTTTATATTACTTTTTTAGTTTGATACTAAGT  
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

0998544.10161

## **FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFEVTVILFFILL  
YVLRLDRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCCLAD  
GALIYRKLLFNPSGPYQKKPVHEKKEVL

### **Important features:**

**Potential type II transmembrane domain:**

amino acids 26-42

**Other potential transmembrane domain:**

amino acids 44-65, 81-101 and 109-129

**Leucine zipper pattern**

amino acids 78-99 and 85-106

**N-myristoylation site.**

amino acids 110-115

**Ribonucleotide reductase large subunit protein**

amino acids 116-127

FIGURE 70

## FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTGCTATCGTTTTGCAGAACC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA  
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTTATNATCGCACAAGCCCC  
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATACTTTTAT  
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC  
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

103107 4453460

## FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG  
CTGGGCGCGCCCCCGGGCCCCGCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC  
CTCTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG  
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCC  
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG  
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC  
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTIONTTGACACAGAGAGGT  
CTAGCACATAACGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG  
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA  
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATAC  
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC  
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC  
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT  
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG  
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC  
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG  
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTTCTGGACTGGGTCCCAG  
CTGGCGTGCTGGACGAATTTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT  
GAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTACATTCAGC  
CCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCATCCACAAAT  
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA  
GAGGGTGGGCTTCGAGCGAGCCCCGTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG  
CCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT  
AATCGTCTCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCA  
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA  
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG  
CTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTAC  
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA  
AAAAAAACTTCATTCTAA

## **FIGURE 73**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPCTPAERHADGLAL  
ALEPALASPAAGANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS  
YIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESNF  
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS  
LVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLR  
LPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISITLRLDENSRSFR  
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFASPCA  
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCGAILLVLLVLLLPFRC  
QRRPRDPEVVNDESSLVRHRWK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 466-494

#### **N-glycosylation sites.**

amino acids 170-173 and 366-369

#### **Leucine zipper pattern.**

amino acids 10-31 and 197-118

#### **Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

## FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG  
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCTGGGCGGGAGCCGGGAGGCGCGGCC  
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA  
CAACCTGGTGAAGGCCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCCGCACGGCCGTGG  
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG  
CGCGTGGTGTGCTGGCCTGCCGCAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA  
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC  
GGGCCTTTGCCACTGCCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC  
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACCTGCTGCTTCGGGTGAACCATAT  
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCTGAAGGCATGTGCCCCTAGCCGCG  
TGGTGGTGGTAGCCTCAGCTGCCCACTGTCGGGGACGTCTTGACTTCAAACGCCCTGGACCGC  
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT  
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC  
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTTGATGGCTGCGCCCACTTTTG  
CGCCCATTTGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG  
TGCTCTACAAGAGGGCATCGAGCCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG  
AGGTGCCTCCAGCTGCCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG  
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC  
AGAGGCCCCATCTTCTCTAAGCACCCCCCACCTGAGGAGCCCACAGTTTCTCAACCTTACC  
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG  
CCTGAGATCCAGCTCTCTTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT  
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC  
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT  
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT  
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG  
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG  
TGAAC TGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCCATGTTAATGAAGCG  
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG  
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA  
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG  
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCTCGGAATAAAGCGCGTTGACCGCCAAAA  
AAAAAAAAAAAAAAAAAAAA

## **FIGURE 75**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGKMTALELARRGAR  
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG  
ISSCGRTREAFNLLLRVNHIGPFLLTHTLLLPCLKACAPSRVVVVASAAHCRGRLDLDFKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFRLRHVPGWLRPLLR  
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDDDRAAHLWEASKRL  
AGLGPGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSPQSSPDLSKMTHRIQAKVEP  
EIQLS

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Glycosaminoglycan attachment site.**

amino acids 46-49

#### **Short-chain alcohol dehydrogenase family**

amino acids 37-49 and 114-124

T09T0T"445B/660



## FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG  
GACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCAGGGCCCTGGCCCTGCCAGGATGAGCTGC  
CAAGCCTCAGGCCAGCCACCTCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCTGAGCATGGTGCCCCCAGAC  
CCACACCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACGATGGCCAG  
GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAAGAGGGCGCT  
CGGCTGTCTGTGGCTGTCTCCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG  
TTTACTCTGGAATGTGGGCCGCCCTGGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG  
GCCCTCCAGCCCCGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG  
ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCCGGGTTTCCATCCAGGAGCCC  
CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAAATGTGACACTGCTGAACCCGGAT  
CCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAAGGTCACTGGCCCTGCTGCGCCTGCCCAA  
TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC  
GGCTGGCAGAGCGCAGAGCTTGGAGGCCTCCACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC  
CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGGAAGAAAGTGCCAGTGCCCCACCTCAGGAA  
GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCAATGGCATC  
ATCCGTGGCTACCAAGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAACCTGGACTGTAGTTGGTGAGCAG  
ACCCAGCTGGAAATCGCCACCCATATGCCAGGCTCCTACTGCGTGCAGAGTGGCTGCAGTCACTGGTGCTGGAGCT  
GGGGAGCCAGTAGACCTGTCTGCCTCCTTTTAGAGCAGGCCATGGAGCGAGCCACCCAAGAACCAGTGAGCAT  
GGTCCCTGGACCCTGGAGCAGCTGAGGGCTACCTTGAAGCGGCCTGAGGTCAATGCCACCTGCGGTGTTGCACTC  
TGGCTGCTGCTTCTGGGCACCGCCGTGTGTATCCACCGCCGGCGCCGAGCTAGGGTGACCTGGGCCCAGGTCTG  
TACAGATATACAGTGAGGATGCCATCCTAAACACAGGATGGATCACAGTGACTCCAGTGGTTGGCAGACACT  
TGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCAGCAGCCTCAGCAGTGGCTGGGGCGGATGCCCGG  
GACCCACTAGACTGTCTGCTCGCTCCTTGCTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCCCTGCTTCCAGACACC  
AGCACTTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCCAGGTCCCAGCT  
GTCAGGCGCCTCCCACCCAGCTGGCCCAGCTCTCCAGCCCTGTTCCAGCTCAGACAGCCTCTGCAGCCGAGG  
GGACTCTCTTCTCCCCGCTTGTCTCTGGCCCTGCAGAGGCTTGGAAAGGCCAAAAAGAGCAGGAGCTGCAGCAT  
GCCAACAGTTCCTCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCCTGTGAGTTAGGAAATAGAGGTTCC  
AAGAACCTTTCCCAAGCCCAGGAGCTGTGCCCAAGCTCTGGTTCCTGGCGGGCCCTGGGACCCGAAACTCCTC  
AGCTCCTCAAATGAGCTGGTTACTCGTCACTCTCCCTCCAGCACCCCTCTTCTCATGAAACTCCCCCAACTCAG  
AGTCAACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCTCCATCCTGCTGCCAGCAGCCCCCATCCCCATC  
CTTAGCCCCCTGCAGTCCCCCTAGCCCCCAGGCCTCTTCCCTCTCTGGCCCCAGCCAGCTTCCAGTGCCTGTCC  
AGCTCCTCACTGTCACTCCCTGGGGGAGGATCAAGACAGCGTGTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA  
CTCAGTGAGGGTGAGGAGACTCCAGGAACAGCGTCTCTCCCATGCCAAGGGCTCCTTCACCCCCACCACCTAT  
GGGTACATCAGCGTCCCAACAGCCTCAGAGTTACGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCCCAAGGGG  
GGAGTCTTGCTGTGCCACCTCGGCCCTGCCTCACCCCCACCCCCAGCGAGGGCTCCTTAGCCAATGGTTGGGGC  
TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCTTGTGAGTCTCTCCGATGGCTCCTTCTCGCTGAT  
GCTCACTTTGCCCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTTGGTTTCGGTCTAGAGCCCAGGGAGGCAGACTGC  
GTCTTCATAGATGCCTCATCACCTCCCTCCCCACGGGATGAGATCTTCTGACCCCCAACCTCTCCCTGCCCTG  
TGGGAGTGAGGCCAGACTGTTTGAAGACATGGAGGTCAAGCCACCCAGCGCTGGGAAGGGGGATGCCTCCC  
TGGCCCCCTGACTCTCAGATCTCTTCCAGAGAAGTCAGCTCCACTGTCTGATGCCAAGGCTGGTGCTTCTCCT  
GTAGATTACTCTGAACCGTGTCCCTGAGACTTCCAGACGGGAATCAGAACCCTTCTCCTGTCCACCCACAAG  
ACCTGGGCTGTGGTGTGTGGGTCTTGGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG  
TTCTCCCTCCACGATTGTGAAAACAAATGAAAACAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAAA  
ACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCCACCACAGGTTGTTTTGGC  
CTGAGGAGCAGCCCTGCCTGCTGCTCTTCCCCACCATTGGATCACAGGAAGTGAGGAGCCAGAGGTGCCTTT  
GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGAGCCCCCTCTCAGCCTTACCT  
GGGCCCCCTCCTCTAGAGAAGAGCTCAACTCTCTCCCAACCTCACCATGGAAAGAAAAATAATTATGAATGCCACTG  
AGGCACTGAGGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGAGG  
TATGAGACCGTAGGTCAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAAATTTGATAACCATAAAAT  
GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 77**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP  
DGTLILLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM  
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMCV  
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV  
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG  
PDSNVLLLRLEKVPSPAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP  
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPD  
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD  
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST  
FYGSLIAELPSSTPARPSPQVPAVRRRLPPQLAQLSSPCSSSDSLCSRRLSSPRLSLAPAEA  
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS  
SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPPSPQASS  
LSGPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY  
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWGSASEDNAASARA  
SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVFIDASSPPSPRDEIFLTPNLSLP  
LWEWRPDWLEDMEVSHTQRLGRGMPPWPDPDSQISSQRSQLHCRMPKAGASPVVDYS

### **Important features:**

#### **Transmembrane domain:**

amino acids 448-467

#### **N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

#### **N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

#### **Phosphotyrosine interaction domain proteins**

amino acids 740-753

TOPTOT 44582660

## FIGURE 78

CTCCACGGTGTCCAGCGCCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT  
CCCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT  
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTTGTGACCCTGTGGA  
ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG  
TCTTTACTGATCTCTCTGTTCTGTTTCCAGGACCCTGCTGTCTCTCCCTCCCCTTCTCCCAC  
CTTCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC  
CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
GCTGAGGCCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCCCCCCCCCATGCAGC  
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
GTGTCCATCCCAGTGGTCCGCATACTGGCCCCAGTCTGGTGCTGCTGAGCCTTCTGTTCAGC  
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA  
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC  
CCTTCCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA  
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT  
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG  
TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCAGGCTCTCCTCTTGTCATGTTCCA  
GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA  
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC  
CTCATGCCCAGTGTGCGACCCCTGCCTTCTCCTCCACTCCAGACCCACCTTGTCTTCCCTCCC  
TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT  
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT  
GTGAAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG  
GACTCTGAATTCTAACAATGCCCAGTGACTGTGCGACTTGAGTTTGAGGGCCAGTGGGCCTG  
ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC  
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG  
TCCAGGCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG  
TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCTTTGGAAAAAATGATGAAGA  
AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTTACTTGCTTATGGGTTCTGGTGGCTAGAGA  
GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA  
GCACAATACTATTTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT  
GCTGCCCAGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCCGCCTCCTGGGTTCAAGTGATT  
CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT  
TTTGTACTTTTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCTGAC  
CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG  
TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTTCAGTATGCAAACTTGGAAG  
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT  
TATTTTCGTTTTGTTGTACTTCCCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT  
TTTACAGAGCAATTATCTTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTTCATCA  
GCTGCATAAAAAAAAAAAAAA

## **FIGURE 79**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGP EEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLODAGEYWCGVEKRGPD ELLISLFV  
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG  
TSQYGHERTSQYTGTSPHPATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD  
VISMPPLHTSEEEELGFSKFVSA

### **Important features:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 248-269

#### **N-glycosylation site.**

amino acids 96-99

#### **Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

#### **Ig like V-type domain:**

amino acids 13-128

FIGURE 79

## **FIGURE 80**

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC  
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA  
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTATCCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG  
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAAC TGGCCAGAGTG  
CTACATGACTTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC  
TTATTTTACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTTCCAGATCAACAGCCGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC  
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC  
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC  
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTTAGGATGGACGGAACCATGCA  
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA  
AAGGATGGTTGAACGTGAAA

097544-10101  
T09T0T"44582650

## FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD  
YEADGSTNNGIFQINSRRWCSNLTNPVNPVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGY  
WEAWRHHCQKDLTEWVDGPDF

**Important features:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 67-72

**Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

0978544-10101

## FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCCTGCGTTC  
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA  
AGCTGTCGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC  
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAAGTCTCCACAC  
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG  
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGACAGTGGGGAGCT  
GGAGAAGTGCGGCTGTGACAGGACAGTGATGGGGTCAGCCACAGGGCTTCCAGTGGTCAG  
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG  
GAAGGCCATCCTGACACACATGCGGGTGGAAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG  
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG  
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC  
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGCCGCACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA  
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGCTGCTTCGTCAAGTGCCGGC  
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCCTGCCTAGCCCTGCGCCGGC  
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA  
GATACTGGTTGTATTTTTTGTCTGGTTTGGTTTTTGGGTCCTCATGTTATTTATTGCCGAA  
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT  
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT  
TACCACCACATGGCTACTGACCGTGTATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA  
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACTCTCCAGCACACA  
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG  
GAACAAGCAGATAACCAGGTCAAGGGCACCAAGGTTCATTTAGCCCTTACATGGACAGCTAGA  
GGTTCGATATCTGTGGGTCCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA  
GTCCACCCCTAGAACCCAGCCTGCCCCAGCCTGCCCCCTGGGAAGAGGAACTTAACCACTCC  
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT  
TGCAGTCATGCCCCAGTCACCTTTCACAGCGCTGTTCTCCATGAACTGAAAAACACACAC  
ACCTGCGAGA  
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCTC

## **FIGURE 83**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRVQMCKRNLE  
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPFGKVVTQGTREAAFVYAISSAGVAFV  
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM  
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR  
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC  
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 88-91 and 297-300

#### **Wnt-1 family signature.**

amino acids 206-215

#### **Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174



## FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT  
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC  
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC  
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG  
GTGCCCTGAAGGAGGAGGTCTGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG  
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT  
GCGGGAAGTGCCTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCTGCGAGCCG  
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC  
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG  
GCTGTGCGCCATCTGGGCAAGGTTCAAGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT  
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGC  
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG  
AAAAGGCACAACTGCTTGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTCGAGCATGTCGTA  
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCCT  
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC  
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC  
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA  
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

## **FIGURE 85**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSSEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA  
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR  
ELRERVVTQGLAEAGRGREDEVRTLEFRALEAVRLQNNSCEPCPTSWLSFEGSCYFFSVPKTTW  
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS  
HWNQGEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 31-54

#### **N-glycosylation sites.**

amino acids 73-76 and 159-162

#### **Leucine zipper pattern.**

amino acids 102-123

#### **N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

#### **C-type lectin domain signature.**

amino acids 264-287

09544-1050  
T0910T-44584650

## FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTGCTGGGCAGGGCGAGTTGGGAAAGCG  
GCAGCCCCCGCCGCCCCCGCAGCCCCTTCTCCTCCTTTCTCCACGTCCTATCTGCCTCTCG  
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACCTGGAGCCTCATTGGCCGGCCCGG  
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC  
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAACCCAGCCCGGCCCGCCCTGGGCAAG  
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGCCAGCCTCTTGGGGGAGAGTC  
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA  
CGGCCTTCCCCAAGCAGTACCCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG  
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTGCG  
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG  
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGTCCCAGCGGCACCGGGCAGACG  
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTTGTGGTGCGCATCGTGCC  
CAGCCCCGACTGGTTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG  
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC  
TCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCCAG  
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA  
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGC  
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAGAAACGCCGCTGGACTGCGAGGTCTC  
CCTGTGGTCTGCTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA  
CTCGCTACGTCCGGGTCCAGCCCCGCAACAACGGGAGCCCCCTGCCCCGAGCTCGAAGAAGAG  
GCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAGAGCCCCGCAGCCCCTGGGGCCCCCGG  
GAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG  
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT  
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG  
CCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC  
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG  
TCCAGGGGCTGGCTCCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG  
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG  
TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT  
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

CGCTTCTCCAG

## **FIGURE 87**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPL  
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDF AERGEAWALMKEIEAAGEALQSVHEVF  
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFGVDSLDCDGRWREQAALDLYP  
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP  
RAFIPPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA  
NNGSPCPELEEEAECVPDNCV

**Important features:**

**Signal peptide:**

amino acids 1-26

0997544"44532660

## FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTGTTGGTGTCCCTGTCTTGCGTGA  
TATTGACAAACTGAAGCTTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA  
CAGCTTTAGTGGCCGGCCGGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC  
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAATA  
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT  
ATCCAACCTTTGTTTGGAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT  
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC  
CATTCAAAGATGAATTTTATTACGGTTGCGTTTTTAATCGGAGAGGACTGGTTGCCATGGCA  
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTGAGCAGATGAACT  
TAACAATAAGCATAACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC  
TGTGAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT  
GAGGTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAGA  
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT  
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG  
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT  
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG  
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAA  
TTAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC  
AGTCAGCCGCGAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAAACGGGAACTCTTAGCAG  
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA  
GCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG  
GAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT  
TTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCTGAAACAGAA  
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT  
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA  
ATAAAAGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAAGAAAGAAGATAAAT  
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG  
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG  
AAAAACAATTATCTTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTTGGTTACTGG  
TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAAATTTTCT  
TCCACAAAAA

## **FIGURE 89**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFI  
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN  
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFNPFDDIIPREIKRLKKEK  
PEEEVKKLKPKGTKNFSLLSFGEEAESEEEEEVNRSQSMKGKSKSSHDLKDDPHLSSVPVV  
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV  
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEEAPPDGAVAEYRREKQKYEALRK  
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK  
DASMQDSDTFEIYDPRNPVNKRREESKKLMREKKERR

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 109-112 and 201-204

#### **Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

#### **Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

099744582660

## FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG  
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTTCGCCTTGCTGACGGCGTGC  
AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC  
GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA  
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG  
CTCCTTCAAGTGGTTTTTGGAAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA  
GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC  
CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCTT  
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAA  
GGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAG  
TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC  
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG  
ATGTACGTGAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT  
GAACGTGTACGCGCCGGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC  
CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCCG  
GAGAAAGTGGTGCTGGTGTCTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA  
CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC  
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTGGGCCAGTCGGCG  
GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC  
CATTTCCAGAGTGGCACCGCGTTATTGAGACTTTTCATCACTAGTAACCCACTGAAAGTGG  
CCAAGAAGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC  
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAAC  
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT  
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGT  
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA  
ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC  
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA  
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC  
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC  
TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA  
TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT  
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC  
TGACATCCCATGATGCCCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC  
ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT  
CCCACCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTGACCCAGACTGCCACTGC  
CCCTGTCACTGCACCCAGCTTGGCATTACCATCCATCCTGCTCAACCTTGTTCTGTCTGT  
TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACTTTTGGTAGTTTGGGA  
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG  
TCTCTTCAATAAAGAAGTGTTGATTAGAAAAA

## **FIGURE 91**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSG  
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVPPFSRPP  
LGILRFAPPEPPEPWKGIRDATTYPPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS  
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVIYAPARAPGDPQLPVMVWFPGGAF  
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA  
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA  
HLACNHNSTQILVNCLRALSGTKVMRVSNNKMRFLQLNFQRPDEEIIWSMSPVVDGVVIPDD  
PLVLLTQGVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD  
IVQDATFVYATLQTAHYHRETTPMMGICPAGHATTRMKSTCSWILPQEWA

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Carboxylesterases type-B serine active site.**

amino acids 312-327

#### **Carboxylesterases type-B signature 2.**

amino acids 218-228

#### **N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

109101"4634660



## FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT  
GCTGTCCTCGCTGCTGGGCGGGTCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG  
AGTCAGTGATGGTGCCGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCGA  
CAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC  
CAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC  
GATTCAGCTCACTGGGGATCCCGCAAGGGGAACCTGCTCCTTGGTGATCAGAGACGCGCAG  
ATGCAGGATGAGTCACAGTACTTCTTTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTT  
CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCAGGACC  
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC  
GTCCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTATCAGCATTTTACGTGACAACAC  
GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCCAAAAGGCCAGT  
TCTTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCGAG  
AACAGAGTCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCCG  
GGTGAAGGCTGGGGATTGAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC  
AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA  
GCAAACAGGACAGTCTTGAAAACCTTGGGAACGGCACGTCTCTCCAGTACTGGAGGGCCA  
AAGCCTGTGCCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA  
GGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGGTCTTGAGCTGCCTCGGGTT  
CAAGTGAGACACGAAGGAGAGTTTACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGT  
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG  
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGGCCCTGATCATCATGAAG  
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAC  
GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA  
AAGCCACACCAAACAGTCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCAGAATCAAAG  
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCCAGAACCCAAATCATCCACTCAAGC  
CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA  
GACCCAGGCCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC  
CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTTCGGCTAGGGAGGAAGGTAGAGTAAGAG  
GTTGAAGATAACAGAGTGCAAAGTTTCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT  
CTCTCTTTCTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC  
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGCGGAGTTGAGACCAGCCTG  
GCCAECTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG  
CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG  
AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA  
TCTCAAAAAAAAAAATCCTCCAAATGGGTTGGGTGTCTGTAATCCCAGCACTTTGGGAGGCTA  
AGGTGGGTGGATTGCTTGAGCCCAGGAGTTGAGACCAGCCTGGGCAACATGGTGAAACCCC  
ATCTCTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCCAGCTGT  
CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC  
TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG  
TACAAGATACAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAA  
ATCCACCAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCGTCTCACTGCTACACTCCT  
GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA  
AAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAA  
GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTTCCTT  
TACTTTCTTAATAAACTTGCTTTTACCTTAAAAAAA

## **FIGURE 93**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYWFK  
AVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPKGNCSLVIRDAQMQDESQYFFRVERGS  
YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS  
ISRDNTPALEPQPOGPNVPYLEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL  
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL  
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP  
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR  
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP  
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Transmembrane domain:**

amino acids 399-418

#### **N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

### **Immunoglobulins and major histocompatibility complex proteins signature.**

amino acids 365-371

109707-1453460

## FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAGCTGTTATTTACTGCTGCGTTT  
 TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA  
 AAGTCAAGCAGCCAGTGCGATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT  
 TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA  
 CAATGGAAACAATTCCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA  
 TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC  
 TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA  
 GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAATTCCTAGATGAACCTTATG  
 AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT  
 GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
 ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC  
 TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
 TCTGGAACAACAAGTGTATTAATTAACCTTTTCTGATGTTAATGACAATAAGCCTATATTTAA  
 AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA  
 TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT  
 GATTGCGAAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTTAAA  
 AAAGAAAGTGGATTTTGGAGCACCAGAACCCTACGGTATTAGAGCAAAAGTTAAAAACCATC  
 ATGTTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTTATTAAAGATCCAG  
 GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTGA  
 AGAAACCCACAGGGATCATTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT  
 CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCATATCAATGATAATGGTACAATC  
 ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC  
 AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGTATGTGCAAGTTCTTAACATCA  
 ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT  
 GGTGAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT  
 TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAGTTTTACAATCATAGATAATCAAG  
 ATAACACAGCTGTCATTTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC  
 TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC  
 CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG  
 TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATA  
 TTTGGGTTTATTTTTTTGACTTTGGGTTTAAAACAACGGAGAAAACAGATTCTATTTCTGA  
 GAAAAGTGAAGATTTTCAAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG  
 ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT  
 CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA  
 CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG  
 CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC  
 CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT  
 GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG  
 GCTTTTTTACCATCAAAATTTTTAAAAGTGCTAATGTGTATTTCGAACCCAATGGTAGTCTTAA  
 AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC  
 CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTCTATTGAACAGAGATGTG  
 GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTGGAAGTAAATAATG  
 TAGGAAGATATTTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT  
 CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG  
 CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA  
 ATTGAAAATGTATAGTCAGAGAAAATTTTCATGAATTATTCATGAAGTATTGTTTCCTTTAT  
 TTAAA

T09T07-14582660

## **FIGURE 95**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH  
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT  
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL  
LYSLLQGQPYFSVEPTTG VIRISSKMDRELQDEYVWIIQAKDMIGQPGALSGTTSVLIKLS D  
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE  
TQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL  
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA  
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR  
DESIEEHFFYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP  
SLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ  
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY  
RQSLQVGPD SAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGS LAGSLSSLES AVSDQD  
ESYDYLNELGPRFKRLACMFGSAVQSNN

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 597-617

#### **N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

#### **Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTTNTA  
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTTCAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTGCGAAACATTTGACATTATT

## FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCCGGGCGCGGACCCCAACCCCGAC  
CCAGAGCTTCTCCAGCGGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTTCCCTCCGCGGGG  
CCCAGCCACCTTCGGGAGTCCGGGTTGCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCA  
CCCCTGAGCCAGCGCGGGCCCCCGAGCGAGTCAATGGCCAAACGCGGGGCTGCAGCTGTTGGGC  
TTCATTCTCGCCTTCCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG  
GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA  
TGTCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT  
CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT  
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC  
AGAAGATGAGGATGGCTGTCAATTGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTA  
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCAGT  
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCC  
TTCTGGGAGGTGCCCTACTTTGCTGTTCCCTGTCCCCGAAAAACAACCTCTTACCCAACACCA  
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACACAGAGGCCAAAAG  
GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAACATTAGGAC  
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAAAA  
ACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTCTCTCA  
ATATAGGAGGGAAGATTTTCCATTTGTATTACTGCTTCCATTGAGTAATCATACTCAAAT  
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTA  
ATAGACAGTAAATACTATTCTCATTATGTTGATACTAGCATACTTAAATATCTCTAAAT  
AGGTAAATGTATTTAATTCCATATTGATGAAGATGTTTATTGGTATATTTCTTTTTCGTCC  
TTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCCTTTG  
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCCTTCAATTCTTCATGCGTGCCCTTTT  
CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT  
TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTCATAGCCTACATTTTA  
GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACTTTGGAGGCAAATCTTTCTGCATG  
ACCAAAGTGATAAATTCCTGTTGACCTTCCACACAATCCCTGTACTCTGACCCATAGCACT  
CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT  
AACACAACCTTATTGATTGAATTTTAAAGCTACTTATTCATAGTTTTATATCCCCCTAACT  
ACCTTTTTGTTCCTTCCCTAATTGTAATTGTTTTCCCAAGTGTAATTATCATGCGTTTTA  
TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA  
ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTCTACCTCTTTT  
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA  
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTTGCT  
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT  
CACTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACTTCAT  
GTGGTTCACTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC  
CTTCATGTGGCTCAGTGCCTTCCTCTCTCTACCAGTCTATTTCCATTCTTTCAGCTGTGTCT  
GACATGTTTGTGCTCTGTTCCATTTTAACTGCTCTTACTTTTCCAGTCTGTACAGAATG  
CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG  
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGGAGCAAGGCATTTGGCTGCTGTAA  
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCCACCTCACAGTGATG  
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAAGTGCTAT  
ACTAAGGGAAAGAATTGAGGAATTAAGTGCATACGTTTTTGGTGTGTGCTTTTCAAATGTTTGA  
AAATAAAAAAATGTTAAG

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI~~L~~AF~~L~~GWIGAI~~V~~STALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQI  
QCKVFDSL~~L~~NLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDDEVQKMRMAVIGGA  
IFLLAGLAILVATAWYGNRIVQEFYDPMTPVNARYEFGQALFTGWAAASLCLLGGALLCCSC  
PRKTT~~S~~YPTPRPYPK~~P~~APSSGKD~~Y~~V

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

#### **N-glycosylation site.**

amino acids 72-75

#### **PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

#### **ABC-2 type transport system integral membrane protein**

amino acids 119-133

TC9TDT"44534660

## **FIGURE 99**

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC  
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC  
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC  
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN  
CNTTCAACANTTCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA  
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT  
GTTCTGTCCC

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC



## **FIGURE 100**

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG  
GCTTCATTCTCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG  
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG  
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA  
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAGGTCTGGCTA  
TTTGTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

## **FIGURE 101**

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC  
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANCACCGGGCAGATCCAGTGCAA  
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT  
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT  
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTT  
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT  
TCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTTGCGA

097544-10101

## **FIGURE 102**

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC  
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT  
GCNTGTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC  
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC  
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCAGTCAATG  
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG  
GGAGGTGCCCTACTTTGCTGTTCCCTGTCCC

609107"44582650

## FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG  
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCCAGTCAATGCCAGGTAC  
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC  
CCTACTTTGCTGTTCCCTGTCCCCGAA

097544 10101  
T09T0T"44582660

## FIGURE 104

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC  
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGC  
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA  
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT  
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA  
ATTTTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG  
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTGCGAACC

## **FIGURE 105**

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA  
CTTTGCTGTTTCCTG

095844-10582660

## **FIGURE 106**

TTCCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC  
TGGCGAACAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC  
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT  
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG  
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGACAGGTCTGGCTATTTTAGNNGCCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCAGTCAATGCCAGGTA  
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG  
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

## **FIGURE 107**

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA  
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA  
TGTACGAGGGGCTGTGGATGTCNGCGTGTTCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACNTGCCTTGATGGTGGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG  
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC  
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT  
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC  
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTTCCTGCGAA



## FIGURE 108

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC  
CGCGTAGACCGACCCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCCCG  
ACCGGTCCCCGCCTTTTGTAAAACCTTAAAGCGGGCGCAGCATTAAACGCTTCCCGCCCCGGT  
GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGCTAAGGAACATGCGGAAGGTGGAG  
CAGGTCTGAGCCTCGAGCCGCAGCACGAGCTCAAATTCGAGGTCCCTTCACCGATGTTGT  
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA  
CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT  
AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT  
TATGGTTTCAGTCTATGTTTGCTCCAACCTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG  
CAAAACCGGAAGACCTTATGGATTCAAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT  
GATAAACACATGATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAAGACAGAAAC  
ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG  
AAGAATGTAAGAGGCTGCAAGGTGAAGTTGAGAGGCTACGGGAGGAGAACAAGCAGTTCAAG  
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTACGATTAGC  
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTTGTCTTTA  
TCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAAGGTTAGCATGCACAGGATGTTAAATTG  
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT  
AATGTATGATGACATCTCACAGGTCTTGCTTTAAATTACCCCTCCCTGCACACACATACAC  
AGATACACACACAAAATATAATGTAACGATCTTTTAGAAAAGTTAAAAATGTATAGTAACTG  
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT  
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC  
TCTTAAATGACACCCCTTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT  
GCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTG  
CTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA  
AGCCCAAAGGAATTGCACCTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT  
TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCCTTAAAGGGACCAA  
GCTAAATTTGTATTGGTTTCATGTAGTGAAGTCAAACCTGTTATTTCAGAGATGTTTAAATGCATA  
TTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTACAAAGAGTACAGTTAATGC  
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT  
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA  
GGAAGTGTTTTTTCTGGGTGAGTAAATAACAACCTGTATAGGGAGGGAAATTCTCAGTAGTG  
ACAGTCAACTCTAGGTTACCTTTTTTAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA  
CCACCTCTCAACCATTACTCACACTTCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC  
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC  
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC  
TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA  
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCCCCAAAATTAAGAAAA

## **FIGURE 109**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID  
AGASINVSVMLOPFDYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRVFE  
LPAENDKPHDVEINKIISTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE  
NKQFKEEDGLRMRKTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

### **Important features:**

#### **Transmembrane domain:**

amino acids 224-239

#### **N-glycosylation site.**

amino acids 68-71

#### **N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

## **FIGURE 110**

GTCAGTCTTCTAGATTGTCCTTATCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG  
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC  
CCAAAATTAAGAATTCTTTTGTCAATTTTGTACATTTGCTCTATGGGGGAATTATTATTTT  
ATCATTTTTATTATTTTGGCATTGGAAGGTAACTTTAAAATGAGC

44584660

## **FIGURE 111**

TATTGTAAAGGCCATTTTAAACCATTTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNNTTCCTCGCCTGTTGGTGCTGGCCNNTTGGGGAGCTGGAGCCCCAGCATGCTG  
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT  
CCGTGTCCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA  
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT  
AAATTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTATTCAGAGATGTTTAATGCATATTTA  
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

## **FIGURE 112**

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA  
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT  
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG  
AAAGTTAAAAATGTATAGTAAC

FIGURE 112

## **FIGURE 113**

GGTGGCCCATTCCCGGCCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC  
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT  
GCTTTGTTCANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACG  
TTATTCAGAGATGTTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA  
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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## **FIGURE 114**

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG  
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC  
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGTATTTCAGAGATGTTTAATGC  
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA  
TGCTGCGTGC

05978544-101501

## **FIGURE 115**

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACNTGNGT  
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC  
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN  
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANCCCC  
GGCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA  
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA  
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTTANTT  
AAAGGGNCCAAGNTAAATTTGTATTGGTTTATGTAGTGAAGTCAAANTGTTATTTCAGAGATG  
TTTAATGCATATTTAANTTATTTAATGTATTTTATNTCATGTTTTCTTATTGTCACAAGGGT  
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG



## **FIGURE 116**

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC  
CACGTGGCCCACTCCCGGCCAGGCTGCTTTCCGTGTCCTTCAGTTCTGTCCAAGCCATCAGC  
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG  
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC  
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA  
CTGTTATTCAGAGATGTTTAAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTC  
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT  
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

## FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA  
GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC  
CTCGGGGACCAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTCAGTGCCA  
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA  
CTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGATATTTTACC  
CCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA  
GGTACCCCGGATTGTGAGTGAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG  
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC  
CTTTCTGAATTGGAGGATTATCTTTCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT  
AACCAGGGTGAAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG  
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTCAGCATCTTGACAAA  
AGGTTCTTAACCAATTTCCCTTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT  
TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTCATGATGGAAAGGACTATG  
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG  
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC  
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGGTC  
AGAGGATTGCCGAAGGGAGGCCTTCCTTTTCAGTGGACCCGGGTCAAGAATACCCACATTCCG  
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGACTATGACTATGCTCTTCTGGA  
GCTGAAGCGTGCTCACAAAAGAAATACATGGAACCTGGAATCAGCCCAACGATCAAGAAAA  
TGCCTGGTGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT  
CGGTTTTGCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC  
GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAGAAATTGGAAGC  
GCAAAATCATTGCGGTCTACTCAGGGCACCAAGTGGGTGGATGTCCACGGGGTTTCAAGAGGAC  
TACAACGTTGCTGTTTCGCATCACTCCCTAAAAATACGCCCAGATTTGCCTCTGGATTACGG  
GAACGATGCCAATTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA  
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT  
GAACTCTGTCAATAGCATTTCACATTTTTTCAAAATCAGGAGATTTTCGTCCATTTAAAAAA  
TGTATAGGTGCAGATATTGAAACTAGGTGGGCACCTCAATGCCAAGTATATACTCTTCTTTA  
CATGGTGTGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT  
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC  
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA  
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA  
CTCTGAGATGGATCCATTTCAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT  
GGGACATTTAGTTTGTGTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA  
CAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA  
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTGAAGAAAGGAAAGCTGAGACATTT  
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG  
AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT  
TCTATGTATGAGGTGCTACATTTTGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT  
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG  
TAATTTTAGATATGTCCTTTCTAAAAATGAATAAAATTTATGAATATGA

## **FIGURE 118**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLLWLIFFTPGLTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC  
GIECQKELPTPSLSELEDYLSYETVFEENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV  
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAHCVHDGKDYVKGSKKLRV  
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKSGRGQRIAEGRPS  
FQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS  
GFDNDRADQLVYRFCSVSDSNLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG  
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

#### **Glycosaminoglycan attachment site.**

amino acids 236-239

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 165-170

## FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG  
ATCCAAGCATGGGAATGCTGCCGTCTGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC  
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG  
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCCAACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTATGAATGGCTTCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA  
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA  
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT  
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCCTTGTCTTAAAAGGTCTTGATCACTT  
ATATCTGGAACCAAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA  
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTCTGTAACCTCGGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC  
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCCCTTCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC  
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCA  
TGTCACTTTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT  
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA  
AACCCAAAGAGAAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTCTAGAGGAGCCCTCGTAAAGTTGTAAAAGCACAGACTGTTCTATA  
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA  
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA  
AAAAAAAA

## **FIGURE 120**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLS  
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPSCLKCQ  
AKGTTLVVELAPKVLDTGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR  
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDLHYLETCTLQGTKGENSLSSSTGTFL  
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP  
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD  
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI  
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK  
EKLPVEAKLPWFKQAQEEGA AVSEEPS

**Important features:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

## FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGCGTGGGCCCTCGGGCCTGAC  
AGATGGCACTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG  
GCCCCCGGTTCTGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT  
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG  
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG  
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGT  
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG  
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG  
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA  
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGGACTCCTCAAAAGTTCAGCTCCCAGCA  
GGATTGTGGTAGTTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAACCTGGCTAACATTCTTTT  
TACCAGGGAAGTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG  
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC  
AATTTGGTGTGATGGGCTTTTTTCAAACCTCCAGTAGAAGGTGCCCAGACTTCCATTTATTT  
GGCCTCTTCACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGGGGATTGTAAAGAGGAAG  
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGAAGTG  
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAATTTTG  
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT  
TGGGATAAGAGAATTTTCAAGAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA  
GTACAATGAAAAATACAATTATATTGTAAAAATTATAACTGGGCAAGCATGGATGACATATTA  
ATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT  
TCATGGCCAAAGTGTTAACTAGTTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC  
CTGGTGTGTGCACACAAGTCTTACTTGGAATAAAATTTACTGGTAC

## FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE  
LLRLGARVIMGCRDRARAEAAAGQLRREL RQA AECGPEPGVSGVGELIVRELDLASLRSVRA  
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHLGHFLLTNLLLGLLKSSAPSR  
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSR SKLANILFTRELARRLEG TNVTVNVLHPG  
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE  
LLPKAMDESVARKLWDISEVMVGLLK

**Important features:**

**Signal peptide:**

amino acids 1-21

**Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

**N-glycosylation site.**

amino acids 212-215 and 239-242

109707-44592660

## **FIGURE 123**

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAAGCTTGTTACT  
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG  
TTACTGAAAAATTATTTTGGGATAAGAGAATTTTTCAGCAAAGATGTTTTTAAATATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA  
AGCATGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTTACTACAATGTTTGGTGTT  
TGTGTGGAAATTATCTGCCTGGCTT

0597544-10160  
T09T0T-44582650



## FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCC  
CTTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC  
CCCAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT  
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACCTGAAATAACAAGTCTTGCTACAGAGA  
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT  
CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT  
TCCAAATGAAAATCAAGTAGTGTGGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC  
AGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAG  
AGAGAATACAGGGGTGAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG  
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAA  
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCG  
AATATTTTGCATGATGACTGTGCCTTTCTTCTGCATTTGGGGATGTTTCAAACCGGAAAG  
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT  
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT  
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT  
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC  
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT  
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCTGTAAATCGCTATTGACAGCTTTAG  
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCTTGGAACCTCAAGCAATTCTG  
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT  
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA  
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTTAAAAACTTG  
AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAATAGTAAACCTA  
TATTTTCATAATCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ  
MLHPIFEEASDVIKEEFPNENQVVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYR  
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILH  
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNW IQDKCVPLVREI  
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH  
IQKTPADCPVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG  
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Endoplasmic reticulum targeting sequence.**

amino acids 403-406

#### **Tyrosine kinase phosphorylation site.**

amino acids 203-211

#### **Thioredoxin family proteins**

amino acids 50-66

## **FIGURE 126**

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG  
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

099544-10101

## **FIGURE 127**

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTGCGCCGCNGGAGCCCCGGGTCGAGAGGACNAGG  
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCCTTTCCTAACCC  
AACCCAACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC  
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC  
TTGGGTTTTTACTCCTGTAACAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA  
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTTCGTTTCAGTCAG  
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA  
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA  
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG  
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

## FIGURE 128

GCCCACGCGTCCGATGGCGTTACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTGATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCAT  
CCACGCTTTCTTCTGTGTATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCAGGA  
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG  
GTGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTT  
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTGTCTTGTGGAAAGACTG  
TTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT  
GATTACCTCTGGTGTGACAGGTTTGAACTTGCACTTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTGTTATAGGAACCTGTA  
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCCTCATCTGTC  
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT  
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA  
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG  
TACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTTCCTTTAGT  
GCAATACAATAAACTCTGAAATTAAGACTC

0597544-10150

## FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF  
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA  
FYLLAFFYYLYGMIYVLVSS

**Important features:**

**Signal peptide:**

amino acids 1-20

**Type II transmembrane domain:**

amino acids 11-31

**Other transmembrane domain:**

amino acids 57-77 and 123-143

109101"44532660

## FIGURE 130

ATTATAGCATTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG  
AATCCCCTTGTA TACTCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC  
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTTTGGCATATCATATTTGGAGGTATA  
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT  
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTTATCTTCTAGCATTTTT  
T TACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT  
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

44582650





## **FIGURE 132**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGSLWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRAQLTYPLHTYP  
KEEELYACQRCRLFSICQFVDDGIDLNRKLECESACTEAYSQSDEQYACHLGCQNQLPFA  
ELRQEQLMSLMPKMHLLEFPLTLVRSFWSMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI  
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFRLCLSLNSGWILTTTLVL  
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG  
PLPTKVNLAHSEI

**Important features:**

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site.**

amino acids 90-93

TOGETHER

## **FIGURE 133**

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTTCGC  
TGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA  
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

## **FIGURE 134**

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC  
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCG  
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG  
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG  
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT  
GGTTGCCAGAATCAGCTGCCATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT  
CCGC

## FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCCGGAGGT  
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC  
GTGCGGACTGGCCTCCCAAGCGTGCGGGCGACAAGCTGCCGGAGCTGCAATGGGCGCGGCTG  
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC  
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGATGATTGT  
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA  
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT  
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA  
GTTCTTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA  
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC  
ATTCAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA  
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAACGTGTTTTAAGCCAC  
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACT  
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG  
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG  
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA  
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT  
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC  
AGGATGAGGAAAAACAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCCCTTG  
CATTTTGATGAGAATTCATTTTTTGTCTGGGGATAAAAAAGACACAACTAAAGGAGGA  
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC  
GTCTGTGGGAAAGCTTCAGACTCAGGGTTTGGGCACCTGCTCTGAAGATCTTATTTTCTGAG  
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCCATCTAACCAGACAAGA  
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAACT  
TCAGGAACTTGTTACAGAATATTCATTAAAGAAAAACAAGCTGATATGTGCCTGTTTCTGGAC  
AATGGAGGCGAAAGAGTGGAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA  
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTT  
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG  
GTACAAATTTTAAAGTTTAAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 136**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974

<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAQAQRCFCQVSGYLDDCTCDVETIDRFNNYRLF  
PRLQKLLESDYFRYYKVNLRPCPFWNDISQCGRRDCAVKPCQSDEVPDGIKSASYKYSEEA  
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNPE  
RYTGYKGPDawkIWNVIYEENCfKpQTIKRPLNPLASGQGTSEENTFYswLEGLCvEKRAFY  
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI  
ELRALSKVLPFFFERPDFQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCfKcRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 280-283 and 384-387

#### **Amidation site.**

amino acids 94-97

#### **Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

#### **Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

#### **Interleukin-7 proteins**

amino acids 338-343

FIGURE 136

## **FIGURE 137**

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA  
GGTCTCTGTGTAGAAAAAGAGCATTTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA  
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA  
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG  
CTTAAGAACTTGTATTTTCTCTACTTAATAGAATAAGGGCTTTATCCAAAGTGTTACCATT  
CTTNGAGCGCCCAGATTTTCAACTNTTTACTGGAAATAAAATTTCAGGATGAGGNAAACAAAA  
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATTCA  
TTTTTTTGCTG

## FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGGCAGGATGGGAGGGAA  
AGTGAAGAAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC  
CGATCAGGCATGGAACTCCCCCTTCGTCACTCACCTGTTCTTGCCCCCTGGTGTTCCTGACAGG  
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG  
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC  
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG  
GGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC  
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTAGAGACAGATGGTGTATGGGGGATTC  
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA  
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCTAGAAAGCAAA  
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT  
GCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCCCTCTCTGGTCT  
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA  
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT  
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCCTGGCAAAGGG  
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAGCTCCATGTTTCCTAACAGA  
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG  
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT  
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG  
AGCCAAGATTGTGCCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA  
AATAATAATAATAATAATTACAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA  
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG  
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

## **FIGURE 139**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW

DGPSGDRRGDVYRCVPVGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Cell attachment sequence.**

amino acids 70-73

#### **N-glycosylation site.**

amino acids 98-101

#### **Integrins alpha chain proteins**

amino acids 67-81

09544 10101  
T09T0T" 44582660



## **FIGURE 140**

CACAGTTCCCCACCATCACTCNTCCCATTCCCTTCCAACCTTTATTTTTAGCTTGCCATTGGGA  
GGGGGCAGGATGGGAGGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACCTCCCCTTCGTCACTCACCTGTTCTTG  
CCCCTGGTGTTCTTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT  
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA  
CCAACTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA  
CAGATGGTGATGG

## FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA  
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
AATGCAGACTTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA  
AACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG  
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA  
CATTTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT  
GGTCGTGCCACTGTTTCGTCTGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG  
TGGTCCTCCCAGACACCTTGAAAATAACCAATTACCCCCAGAAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT  
CTCATAGGTTTTGCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC  
ATGAGGGGACAAGTTGTGTTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTTGTCTAACAGAACAC  
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACACAGAGTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG  
TGTTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGAGAGAGCCCACTTTCCAGATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACTTCAAGCCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACTACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTTGTGCTCCTTTTTTC  
TGTTGGTAAAGTACAGAATTGAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAAAAAAA

## **FIGURE 142**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS  
SILKHPFNRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGAEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPLVLALFAFVGFMILILV  
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Transmembrane domain:**

amino acids 230-255

#### **N-glycosylation site.**

amino acids 40-43 and 134-137

#### **Tissue factor proteins.**

amino acids 92-119

#### **Integrins alpha chain proteins**

amino acids 232-262

## FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATT CAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

## FIGURE 144

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA  
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTTTGGCATTGTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT  
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGG  
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGC  
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC  
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA  
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAGGCTCAGCACTGGAGGAGAGA  
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCTCCTTTACAGCCACCGACTCAGTGAAC TGCGGCTGCT  
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG  
AGGTGCAGCTCATTCACTTCAACCAGGAACTCTACGGGAATTCAGCGCTGCCTCCCGCGGC  
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCTC  
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC  
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGC  
AACAGGGACCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGA  
TGGTGTCCCCCATGGTCGCTGAGACTCCCTTCGAGGATTGCACCCGCCCGTCCTAAGCCTC  
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

## **FIGURE 145**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC  
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL  
LYSHRLSELRLLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL  
FVNVASTSNPFLSRLLNDRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSLTPPCSE  
TVTWILIDRALNITSLQMHSRLRLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER  
RCRGPNYRLHVDGVPHGR

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 177-199

#### **N-glycosylation site.**

amino acids 118-121, 170-173 and 260-263

#### **Eukaryotic-type carbonic anhydrases proteins**

amino acids 222-270, 128-164 and 45-92

# SECRET

GGGCGCTGGTTCTCGCGCTACTGGCTGTACGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCCGCCGCCGAGCCTC  
GTTCTGTCTCCCCGCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA  
GCAGCTCCCTTCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGC  
CGCAGAGGCGGAGGCTCGCGTATTTCTTGCAGTACAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTC  
GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCGGTCCGGTTTGGCT  
CACCTCTCCAGGAAACTTACACTGGAGAGCAAAAGGAGTGAAGAGACCTGTCTTGAGAGATTTCTTGGGGAA  
ATCCTGAGGTCAATTCATTGAAGTGTACCGCGCGGAGTGGCTCAGAGTAACACAGTGCTGTTTATGGCTAGA  
GCAATTCAGCCATGGTGGTTCCTCAATGCCACTTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT  
GAGTGGTGGATAGCCAAACAACGAGGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT  
AATAAATTACGAAGTCAGGTGTATCCAAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGAAAGA  
TCTGCAGAATCTTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGTCTTCATCAATTGGACAGAAT  
TTGGGAGCACACTGGGGAGATATAGGCCCCCCGAGCTTTTATGTACAATCGTGGTATGAGAGTGAAGAGCTTT  
AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTCAAGTGTCTGGCCCTGTATGTACACATTATACA  
CAGGTCTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAAATTTGTGTACATAACATGAACATCTGGGGGCGAG  
ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCTTACAAA  
CATGGGCGGCCCTGTTCTGCTTGGCCACCTAGTTTTTGGAGGGGGCTGTAGAGAAAACTGTGCTACAAAGAAGGG  
TCAGACAGGTATTTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAAGCAGACAGCTCAAGTCCATGACACC  
CATGTCGGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCTAAGCGCAGCAGCAAGTGTCCAAATTTGTTCT  
TGTGAAGTAAAGTTAAGAGATCAGTGCAAAAGGAACAACCTGCAATAGGTACGAATGTCCTGCTGGCTGTTTGGAT  
AGTAAAGCTAAAGTTATTGGCAGTGTACATTTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT  
ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTTATTTCAATCAAGTCCAAATAGA  
AATGGTATTTCAAACAATTGGCAAAATATCAGTCTGTCTAATTCCTTTCACAGTCTCTAAAAGTAAACAGTTTCAGGCTGTG  
ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTCTAAGGCTGCTTACATTTGCCAAGAGTATACCTGTCTCT  
CGTAAGCTGTATGCAAGCAAAATCCACATTTAGTCTCGTGTGAAGTGAACCTCGAGTTTTATTCTGATCTGTCCAGTATC  
TGCACAGTCAGCAGTACATGCTGGAGTGGTTTCAAAATCACGGTGGTTATGTTGATGTAATGCCCTGTGGACAAAAGA  
AAGACCTACATTTGCTTCTTTTTCAGAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATTTC  
AGAGTGTGTTGCTGTTGTGTGAAGTGAATCTTGAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA  
ATTTTGTATAAAACTGTAACATTACTGTACAGAGTACATCAACTATTTTCAGCCCAAAAGGTGCCAAATGCATA  
TAAATCTGTATAAACAAGTCTATAAAATAAACAATGGGACATTAGCTTTTGGGAAAGTAATGAAAATAAATGG  
TTTTAGAAATCCTGTGTTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTCAGAGTTAATTACATAGTCATGATT  
GTTCTACGTTTCATATATTATATGGTGCCTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG  
GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAAACCTGAAAGAAACCTTATCACATTTTCCCC  
AGTTCAATGCTATGCCATTACCAACTCCAATAATCTCAAATATTTTCCACTTAAATAACTGTAAAGGTTTTTTTTTC  
TGTTAATTTAGGCATATAGAAATTTAAATTTCTGATATTTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC  
CAAAATGAATCTGTTTAAATGTTTGAATTTCTTGGGAATGGCCTTAAAAATAAATGTAATAAGTACAGATGGTGGT  
ATGAAAACATTCTTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTCTATGTACTGTTA  
AAATTGAGGTACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT  
GAACAAAGATGAACATAATGTATTACATTACCATTGCCACTGATTTTTTTTTTAAATGGTAAATGACCTTGTATATAA  
ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGTATTGTGCTTTTGATACTAAA  
AATCTGTAAATGTTAGTTTTTGGTAATTTTTTTCTGTGGTGGATTTACATATTAATTTTTTTCTGCTGGTGGAA  
TAAACATTAAATTAATCATGTTTTCAAAAAA

## **FIGURE 147**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDM  
QSILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW  
GRYRPPTFHVQSWYDEVKDFSYPEHECNPYCPFRCSGPVCTHYTQV VWATSNRIGCAINLC  
HNMNIWGQIWPKAVYLV CNYS PKGNWWGHAPYKHGRPC SACPPSFGGGCRENLCYKEGSDRY  
YPPREEETNEIERQQSQVHDTHVRTRSDSSRNEVIS AQMSQIVSCEVRLRDQCKGTT CNR  
YEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKH YFIKSNRNGI  
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG  
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPG GKAFRV  
FAVV

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

#### **N-glycosylation site**

amino acids 28-31



## FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG  
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT  
GGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGCTCCCTGCTCCCACGCCG  
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGT  
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC  
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT  
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAGCTGC  
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA  
GAATAGGGTGAAAAACCTCAGAAGGGGAAAACCTCCAAACCAGTTGGGAGACTTGTGCAAAGGA  
CTTTGCAGATTAAAGCCTTTC  
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTTACCAACGGTCAG  
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT  
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACCTCATGCCTTTCTTTTTTAA  
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGA  
GGAACAATGAGCTTGGTGGACACATTTCAATTGCAGTGTTGCTCCATTCTTAGCTTGGGAAGC  
TTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG  
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCGTGTAGCCGGGCAAGCAGGAGCAGGTCTCT  
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCT  
GGTTAATTTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC  
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA  
TTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACT  
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT  
TTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT  
GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCC  
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT  
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA  
AAAAAAAAAA

## **FIGURE 149**

MSLLPRRAPPVSMRLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH  
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

**Signal sequence:**

amino acids 1-34

095844 44584660

## FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTTACCCCGGTCTGCGTCATGTTAAACTCCAATGTCCTCCTGTG  
GTAACTGCTCTTGCCATCAAGTTCACCTCATTTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG  
CAAAATCCGGGGCCTAAGAACACCGTTACCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTA  
TGCCCTACCCCCCACTGGAGAGAGGCGGTTTCAGCCCCCAGAACCCCGTCCTCCTGGACTGGCATCCGAAATAC  
TACTCAGTTTGTGCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCCATCTGGTT  
TACCGCCAATTTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTAAACATCTACGT  
GCCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA  
TATTCATGATCAGAACAGTAAGAAGCCCGTCATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACC GGCAA  
CATGATTGACGGCAGCATTTTGGCAAGCTACGGAAACGTCATCGTGATCACCATTAACTACCGTCTGGGAATACT  
AGGGTTTTTTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTGCGGTG  
GATTGAGGAGAAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC  
CTGTGTGACCGCTGTTGACCTGTCCCACTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTCAGAGCGGCACCGC  
CCTGTCCAGCTGGGCAGTGAACCTACCAGCCGGCCAAGTACACTCGGATATTGGCAGACAAGGTCGGCTGCAACAT  
GCTGGACACCCAGCATGCTAGAAATGCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC  
GGCCACCTACCACATAGCCTTCGGGCCGGTGATCGACGGCGACGTCATCCAGACGACCCCCAGATCCTGATGGA  
GCAAGGCGAGTTCTCACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCCCTGAAGTTCTGGACGGCAT  
CGTGGATAACGAGGACGGTGTGACGCCCCAACGACTTTGACTTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGG  
CTACCCCTGAAGGAAAAGACACTTTGCGGGAGACTATCAAGTTCATGTACACAGACTGGGCGGATAAGGAAAACCC  
GGAGACGCGGCGGAAAACCTGTTGGCTCTCTTTACTGACCACAGTGGGTGGCCCCCGCCGTGGCCGCGGACCT  
GCACGCGCAGTACGGCTCCCCCACCTACTTCTATGCCTTCTATCATCACTGCCAAAGCGAAATGAAGCCCAGCTG  
GGCAGATTTCGGCCCATGGTGATGAGGTCCCCTATGTCTTCGGCATCCCCATGATCGGTCCCACCGAGCTCTTCAG  
TTGTAACTTTTTCAAGAACGACGTCATGCTCAGCGCCGTGGTTCATGACCTACTGGACGAACCTTCGCCAAAACCTGG  
TGATCCAAATCAACCAGTTCTCAGGATACCAAGTTCATTACACAAAACCCAACCGCTTTGAAGAGTGCGCCTG  
GTCCAAGTATAATCCCAAAGACGAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGGGC  
AACGAAAGTGCGCTTTCTGGTTGGAACCTGTTCCCTCATTTGCACAACCTTGAACGAGATATTCCAGTATGTTTCAAC  
AACCACAAAGGTTCTCCACCAGACATGACATCATTTCCCTATGGCACCCGGCGATCTCCCGCCAAGATATGGCC  
AACCACCAAACGCCCAGCAATCACTCCTGCCAACAATCCCAAACACTCTAAGGACCCCTACAAAACAGGGCCCTGA  
GGACACAACCTGTCTCATTTGAAACCAAACGAGATTATTCACCGGAATTAAGTGTACCATTGCCGTGCGGGCGTC  
GCTCCTCTTCTCAACATCTTAGCTTTTTCGGCGCTGTACTACAAAAGGACAAGAGGCGCCATGAGACTCACAG  
GCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGCTCACATCCAGAACGAAGAGATCATGTCTCTGCAGAT  
GAAGCAGCTGGAACACGATCAGGAGTGTGAGTCGCTGCAGGCACACGACACACTGAGGCTCACCTGCCCGCCAGA  
CTACACCCCTCACGTGCGCCGGTCGCCAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAA  
CACACTGACGGGGATGCAGCCTTTGCACACTTTTAAACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA  
CGGACATTCCACCACTAGAGTATAGCTTTGCCCTATTTCCCTTCTATCCCTCTGCCCTACCCGCTCAGCAACAT  
AGAAGAGGGAAGGAAAGAGAGAAAGGAAAGAGAGAGAGAAAGAAAGTCTCCAGACCAGGAATGTTTTTGTCCCACT  
GACTTAAGACAAAAATGCAAAAAGGCAGTCATCCCATCCCGGCAGACCCCTTATCGTTGGTGTTTTTCCAGTATTAC  
AAGATCAACTTCTGACCTGTGAAATGTGAGAAGTACACATTTCTGTTAAATAACTGCTTTAAGATCTCTACCA  
CTCCAATCAATGTTTGTGATAGGACATCACCATTTCAAGGCCCGGGTGTTCACACGTCATGGAAGCAGCT  
GACACTTCTGAACTCAGCCAAGGACACTTGATATTTTTTAATTACAATGGAAGTTTAAACATTTCTTCTGTGC  
CACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGGCCAGCATGGAGCTGTAATCCAG  
AGAGAAGGAAACGTAGAAATTTATTATTAAGAAGTGGACTGTGCAGCGAAATCTGTACGGTTCTGTGCAAGAG  
GTGTTTTGCCAGCTGAACTATATTTAAGAGACTTTGT

## **FIGURE 151**

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP  
PTGERRFQPPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMPLIWFTANLDTLMTYVQDQN  
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGYGLLDQIQALRWIEENVGAFGGDPKR  
VTIFGSGAGASCVSLLTSLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCNML  
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV  
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP  
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKPSWADSAHGDEVPIV  
FGIPMIGPTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPVQDTKFIHTKPNRFEEVA  
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMTS  
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTEISVTIavg  
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE  
SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN  
LPHGHSTTRV

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domains:**

amino acids 189-204, 675-692

## FIGURE 152

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCTGTGGCAGCAGTGGCGGCGATGTTTGT  
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGTGTGGGGTCTGGGCAGGGGCCA  
CAGCAAGTCGGGGCGGGTCAAACGTTTGAGTACTTGAAACGGGAGCACTCGCTGTCTGAAGCC  
CTACCAGGGTGTGGGCACAGGCAGTTCTCTACTGTGGAATCTGATGGGCAATGCCATGGTGA  
TGACCCAGTATATCCGCCTTACCCACAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG  
GTGCCATGTTTTCTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAATCCATGGACAAGGAAA  
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC  
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT  
GAGGAGAAGCAGCAAGAGCGGGTATTTCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT  
CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC  
GCAATCTTCATTACGACACCTTCTTGGTGAATTCGCTACGTCAAGAGGCATTTGACGATAATG  
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC  
CCGCGGCTACTACTTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA  
TTTCCTTGAAGTTGTTTGAAGTACAGTGGAGAGAACCCAGAGAGGAAAAGCTCCATCGA  
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC  
CCTGAGTGGCCTGGCCCTCTTCCTCATCGTCTTTTTCTCCCTGGTGTCTTCTGTATTTGCCA  
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA  
GCCCTCCTGCTGCCACCACTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCACTG  
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG  
TCACTGGAGTTTTTGAATGCAGGGACCCCGCATTCCCATGGTTGTGCATGGGGACATCTAACT  
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC  
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC  
AGAATTTCATAGCCAGGCTGCCGTGTTGTTTGAAGTCTCAGAAGGCCCTTCTACTTCAGTTTTG  
AATCCACAAAGAATTAAAACTGGTAACACCACAGGCTTTCTGACCATCCATTCTGTTGGGTT  
TTGCATTTGACCCAACCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAACT  
TCTTCCCTGCCTTACCTTCCTTTCACTCCATTCAATGTCTCTCTGTGTGCAACCTGAGCTG  
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTCAC  
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT  
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG  
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG  
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTCTATGTG  
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT  
TACGATTTTTTGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT  
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTTTCTTAATGGACAAGAGACAGT  
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT  
CACTGTCAATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCACCTGCCTTA  
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG  
AGTCTCCTTGGAGGGCCTGGAACCTGAGTCCTCCTATGAACCTCTGTAGCCTAAATGAAAT  
TCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG  
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

## **FIGURE 153**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSDRGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ  
GVGTGSSSLWNLMGNAMVMTQYIRLTQDMQSKQALWNRVPCFLRDWELQVHFKIHGQGKKN  
LHGDGLAIWYTKDRMQPGPVFGNMDKFFVGLGVFVDTYPNEEKQQQERVFPYISAMVNNGSLSY  
DHERDGRPTLGGCTAIVRNLYHDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG  
YYFGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLPSVDNMKLPENTAPLPPLS  
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

### **Signal sequence:**

amino acids 1-38

### **Transmembrane domain:**

amino acids 310-329

## FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT  
CTGATGGTGGGTGCGTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT  
TGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCT  
GACATGTTCCCGATTTTGAGGTGAAACCATGAAGAGAGAAAATAGAATACTTAATAATGCTTTTTCCGCAACCGCTTCT  
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT  
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCTGTGACGGAGCCCCCTGTGA  
CAGACCCCGTTTTATGAAGCTCTTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTATGCC  
CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTTATTGCCACGGAGACAGGTACCCACTGTATGTCAATCCCA  
AAACAAAGCGACCAAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCA  
TTAGTCACATGTCAAAAGGATCCGGAGCCTCTTTCGAAAGCCCCCTTGAACCTCTTGCCCTCTTACCCAAATCACC  
CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTCAGCTGCTGAGGGATA  
TCTATCTAAAGAAACACAACTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA  
GCCGGACCTTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGAAGTGAAGAAGATTTATTTCA  
GGCACCAGCCAAGTGCCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAGAAACAGTATCTGGAAGAGGAGC  
AGCGTCGTACGTACCTCCTACGTTTGAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG  
ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTCACT  
TTCCCTGTACCCAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA  
GGGAAAGACGGGAGAAGAAATTGTACTTCGGGTATTCTCTCTGGGTGCCACCCCATCTGAACCAAAACCATCG  
GCCGGATGCAGCGTGCCACCGAGGGCAGGAAAGAAGAGCTCTTGCCCTCTACTCTGCTCATGATGTCACTCTGT  
CACCAGTTCTCAGTGCCTTGGGCCTTTTCAAGGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT  
GGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCGGGATTTCTTTACAATGGCGTCGATGTCACTTCCACACCT  
CTTTCTGCCAAGACCACCAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAAACTTGGTCCGCTTTGTGAAAG  
GGGACATGTTTTGTAGCCCTGGGTGGCAGTGGTACAAATTTATTATGATGCATGTACAGGGAAGGATTTCTAAAGG  
TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTTAC  
TAAGGGTAGAAGATTATTGCTTTTTTAAAGGCTAAATATTGTTTGTGGGAACCAAGATGGTTGGGGTTGAACAGT  
AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTTACAGAGGAATAGAAGGTACTT  
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC  
TCTTCTGGCCTGCCCCATGTTACTATGTGATGGAACCAGCACACCTCAACCAAAATTTTTTTAATCTTAGACATT  
TTTACCTTGTCCTTGTTAAGAATTTCTTGAAGTGATTTATCTAAAAATAAAGGTTGGCAAACTTTTTCTGTAAAGG  
GCCAGATTGTAAATATTTTCACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTGCATAACTACTCAACTCTGT  
TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAACA  
GATGGTGACCAGACTTGGCCCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC  
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCTCCAGTAACCTTCTGCTAGAAACA  
CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTTGAATTAGAATGAATCATAGAA  
AACTGATTAGAAGAATACTTGATGTTTTATGATGATTGTGGTACAAGATAGTTTTAAGTATGTTCTAAATATTTGT  
CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAAATATT  
TTCTAAGACCAGTTTTAGATGACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG  
GAGGCTAGAAGATGAATTCAGGCACCTTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA  
ACTGGATTCATTTTTAAACCATTTTCATCAGTTTCAAATGGTAAATTTCTGATTGATTTTTAAATGCGTTTTTGA  
AGAATTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG  
TGATTTCTGAACATAATGGTGCTAATTCAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTCTATCGGCATTCC  
AACTTTTTCTCTTTGTTTTTGTCCAGTGTGCAATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAAGATAA

# THE BIBLE

><subunit 1 of 1, 480 aa, 1 stop

MLFRNRFLLLALLALAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDPVY  
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP  
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK  
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP  
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSM LCHFCHNVSFPC  
TRNGCVDMEHFVKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQITIGRMQRATEGRKEELF  
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSHSVRILYNGVDVTFHTSF  
CQDHHKRSPPKPMCPLENLVRFVKRDMFVALGSGGTNYDACHREGF

amino acids 1-18



## FIGURE 156

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCCATCCCCTTTTGAAGAACAGTACTGTGGA  
GCTATTTAAGAGATAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC  
GCCGCTGTTTACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGCACGCGCCTGAAGCACAAGCAGAT  
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTCTAT  
GGGCGAAGGAACGTCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAATGAT  
TCCTGCGCGACTGCACCGGGACTACAAAGGGCTTGTCTGCTGGGAATCCTCCTGGGGACTCTGTGGGAGACCGG  
ATGCACCCAGATACGCTATTCACTTCCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT  
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGCAGCTTTTCGCCCT  
GAATCCGCGCAGCGGCAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG  
TCAATTTAAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA  
CGACAATGCGCCTTACTTTTCGTGAAAGTGAAATTAGAAAATAAAAATTAGTGAAAATGCAGCCACTGAGATGCGGTT  
CCCTCTACCCACGCGCTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCCGAACACTCA  
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCCTGGACCG  
CGAAGAAAAGGCTGCTCACCACCTGGTCTTACGCGCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCG  
CATCCGCGTGATGGTTCTGGATGCGAACGACAACGCACCGAGCGTTTGTCTCAGCCCGAGTACCGCGCGAGCGTTCC  
GGAGAATCTGGCCTTGGGCACGCGAGCTGCTTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGCGGAAGT  
GAGGTATTCTTCCGGTATGTGGACGACAAGCGCGGCCAAGTTTTCAAAGTAGATTGTAATTGAGGACAATATC  
AACAATAGGGGAGTTGGACCACGAGGAGTCAGGATTTCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATA  
TTCTGCGCGAGCCAAAGTCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCTCACCTCTCT  
CGCCAGCTCGGTTCCCGAAAACCTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGACCAAGATTCTGA  
GGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA  
TAGTTTAGTACAGACATAGTCTTGGATAGGGAACAGGTTCTCTAGCTACAACATCACAGTGACCGCCACTGACCG  
GGGAACCCCGCCCCCTATCCACGGAAACTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCGCGGTCTT  
CCCTCAGGCCTCCTATTCCGCTTATATCCAGAGAACAAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA  
CGACCCCGACTGTGAAGAGAACGCCCAGATCACTTATTCCTGGCTGAGAACACCATCCAAGGGGAAGCCTATC  
GTCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA  
CTTGCAAGTGAAAGTGATGGCGCGGGACAACGGGCACCCGCCCTCAGCAGCAACGTGTGTTGAGCCTGTTCTGT  
GCTGGACCGAAGCACAATGCGCCCCGAGATCCTGTACCCCGCCCTCCCCACGGACGGTTCCACTGGCGTGAGCT  
GGCTCCCCGCTCCGACAGAGCCCGGTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC  
CTGGCTGTCTTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG  
CACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCTCGTAGTGGCCGTCCAGGACCACGGCCAGCC  
CCCTCTCTCCGCCACTGTACGCTCACCGTGGCCGTGGCCGACAGCATCCCCAAGTCTTGGCGGACCTCGGCAG  
CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG  
CGTCTTCTGCGCTTTCGTCTCTGCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCACGCCTGCTGCAGGC  
TTCAGGAGGCGGCTTGACAGGAGCGCGGCGTGCACCTTGTGGGCGTGGACGGGGTGAGGCTTTCTGCGAGAC  
CTATTCCACAGAGTTTCCCTCACACGGACTCGCGGAAGAGTCACCTGATCTTCCCCAGCCCCAACTATGCAGA  
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAGCGAGCCCCCTTTTGTCTGTCAGGTGATTGGGTATTTTCTAAAGA  
CAGTCATGGGTTAATTGAGGTGAGTTTATATCAAATCTTCTTTTCTTTTAAATTGCTCTGTCTCCCAAGC  
TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCTCAAATCCTAGGCTCAAGCAATTATCCACCTTTGCGCT  
CCGGTGTAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTATCTAT  
CTATCTATCTATCTATCTATTACTTTCTTGTAACAGACGGGAGTCTCACGCCTGTAATCCAGTACTTTGGGAGGC  
CGAGGCGGGTGGATCACCTGAGGTTGGGAGTTTGAGACCAGCCTGACCAACATGGAGAAACCCCGTCTATACTAA  
AAAAATACAAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT  
TGCTTTAACCTGGGAGGTGGAGGTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG  
AAACTCTATCTCA

## **FIGURE 157**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVP EELEKGSRVGDISRDLGLEPRELAER  
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR  
DINDNAPYFRESELEIKISENAATEMRFP LPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA  
DGSKYPELV LKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR  
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE  
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTS LASSVPENSPRGTLIALLNVN  
DQDSEENGQVICFIQGNLPFKLEKSYGNYSLVTDIVLDREQVPSYNITVTATDRGTPPLST  
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVS LSVSVTAHDPDCEENAQITYSLAENTI  
QGASLSSYVSINS DTGVLYALSSF DYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN  
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQNAWLSYRLLKASEPGLFSVG  
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVT LTVAVADSIPQVLADLGSLESPA  
NSETSDLTLYL VVAVAAVSCVFLAFVILL LALRLRRWHKSRL LQASGGGLTGAPASHFVGVD  
GVQAFLQTY SHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL  
IEVSLYQIFFLFFFNCSVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRD YRCKPPTVCLS  
IYLSIYLSIYLSIYLLLSCTDGSLTPVIPVLWEAEAGGSPEVGS LRPA

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domains:**

amino acids 693-711, 809-823, 869-888

## FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG  
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC  
ACAGGAGGACAAGGTGCTGGGGGGTTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG  
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAAGTGGCAACTGGGTCTT  
ACAGCTGCCCCTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA  
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG  
CACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA  
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG  
CCCCCTGGTGTGTGATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT  
CTGGTTC

## **FIGURE 159**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL  
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSI PHPCYNSSDVEDHNHDLMLL  
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCED  
AYPGQITDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGSDFCGRSDKPGVYTNICRY  
LDWIKKIIGSKG

### **Important Features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 51-71

#### **N-glycosylation site.**

amino acids 110-113

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

#### **Tyrosine kinase phosphorylation site.**

amino acids 182-188

#### **Kringle domain proteins motif**

amino acids 205-217

## FIGURE 160

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCG  
CGCGCCGCCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCCGCGCCCCG  
GCCCCGCGCCAGGTGAGCGCTCCGCCCCGCGCGAGGCCCGCCCCGGCCCCCGCCCCCG  
CCCCGGCCGCGGGGGGAACCGGGCGGATTCTCGCGCGTCAAACCACCTGATCCCATAAAC  
ATTCATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCGCCGCCCTCG  
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCCAGCCAGAGCCGGGCGGAGC  
GGAGCGCGCCGAGCCTCGTCCCGCGGCCCGGGCCGGGGCCGTAGCGGCGGCGCCTGGA  
TGCGGACCCGGCCGCGGGGAGACGGGCGCCCCGCCCGAAACGACTTTCAGTCCCCGACGCGC  
CCGCCCCAACCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG  
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA  
GCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG  
CTGCCAGCCAGCGCATCTTCTGACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
CGTGCCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGC  
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC  
GGTCTGTGGACCCTGCCACATTCCACGGCCTGGGCCCGCCTACACACGCTGCACCTGGACCGC  
TGCGGCCTGCAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA  
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA  
CACACCTCTTCTGACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTG  
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCTT  
CCGTGACCTTGGCCCGCCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCA  
CTGAGGCCCTGGCCCCCTGCGTGCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG  
TGTGACTGCCGGGCACGCCCACTCTGGGCCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGA  
GGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG  
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC  
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT  
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG  
ACAGCCCGCCGGGCAACGGCTCTGGCCCAACGGCACATCAATGACTCACCTTTGGGACTCTG  
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT  
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCAGCCACT  
GCCGTCTGGGCCAGGCAGGCAGCGGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC  
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT  
TGGGCCCTGCTGAACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC  
GGGGTCTCTCTCCACGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG  
GTCTCTCCCTGATGGACGCCTGCCGCCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG  
TTCGGCGGCAGCGTTTGTTCAGAACGCCGCCTCCACCCAGATCGCGGTATATAGAGATAT  
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA  
AAAA

## **FIGURE 161**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI  
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAAF TGLALLEQLDLSDNAQLRSVDPA  
TFHGLGRLHTLHLDRCLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH  
GNRISSVPERAFRGLHSLDRLLHQN RVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP  
LRALQYLRLNDNPWVCD CRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCA  
VATGPYHPIWTGRATDEEPLGLPKCCQPDAA DKASVLEPGRPASAGNALKGRVPPGDSPPGN  
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA  
GSGGGGTGDSEGS GALPSLTCSLTPLGLALVLWTVLGPC

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Leucine zipper pattern.**

amino acids 135-156

#### **Glycosaminoglycan attachment site.**

amino acids 436-439

#### **N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

#### **VWFC domain**

amino acids 411-425

**Abstract**

GGAAAGTCCACGCGGAGCTTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC  
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCAACAGCCTCAGATACTGGGGACTTTAC  
AGTCCACAGAACCGTCTCTCCAGGAAGCTGAATCCAGCAAGAACAATGAGAGGCCAGCGGGA  
AGCTCATTTGCAGACAAAGGCAAGTCTTTTTTCTTTTCTCTTTTGGGCTTATCTCTGGCG  
GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCAC  
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGTTAGGGTTG  
TTTCCAGAGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT  
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT  
GTTGCTAGAGAGTCCCTTCGAGTTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG  
ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA  
TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACCCGCAAACGCAGTGATGGCAGGAAAT  
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA  
CTCACAGCACTGGATGGTGGCTCTCCGCCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT  
CCTGGATGTCAACGATAATGCCCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG  
AGGACAGTCCGGTAGGCTTCCTGGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC  
AACGGAGAGATTTCTTATTCATTTTTTCAAGCTTCAGAAGAGATTGGCAAACCTTTAAGAT  
CAATCCCTTGACAGGAGAAATTGAACTAAAAAACAACCTCGATTTGAAAAACTTCAGTCCT  
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT  
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT  
ACCTGAGAACGCGCCTGAAACTGTGGTTGCACTTTTCAGTGTTTCAGATCTTGATTCAGGAG  
AAAATGGGAAAATTAGTTGCTCCATTCAGGAGGATCTACCCTTCCTCCTGAAATCCGCGGAA  
AACTTTTACACCCTACTAACGGAGAGACCCTAGACAGAGAAAGCAGAGCGGAATACAACAT  
CACTATCACTGTCACTGACTTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC  
TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCCTACACCCTGTTCTGTC  
CGCGAGAACAACAGCCCCGCCCTGCACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG  
CACCAACGCCCAGGTCACCTACTCGCTGCTGCCGCCCCAGGACCCGCACCTGCCCTCACAT  
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTCTCTGGACTACGAG  
GCCCTGCAGGGGTTCCAGTTCCGCGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG  
CGAGGCGCTGGTGCGCGTGGTGGTGCTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC  
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGCCGGGCTAC  
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTGTACCA  
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTTCGGCGTGTGGGCGCACAATGGCGAGGTGCGCA  
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGCTGGTCAAGGAC  
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC  
CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCCGACCCAGGCCAGGCCGACTTGCTCACCG  
TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGCTCCTGTTT  
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCTCGGTGGGTGCTGCTTGGTGCCTGA  
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCTATCCAGAGCTACC  
AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAGTTCTGAAGCCGATT  
ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA  
TAACTTTGGGTTCAATATTTCAGTGACCATAGTTGACTTTTACATTCCATAGGTATTTTATTT  
TGTGGCATTTCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT  
TTACTCTTGATTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT  
CCTGGTTCTT

## **FIGURE 163**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR  
RGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRVFQVLLES PF EFFQ AELQV  
IDINDHSPVFLDKQMLVKVSESSPPGTTFFPLKNAEDLDVGQNNIENYIIISPNSYFRVLTRKR  
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRS GTAQVYIEVLDVNDNAPEFEQPFY  
RVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS  
DLDSGENGKISCSIQEDLPFLLKSAENFYTLLTERPLDRESRAEYNITITVTDLGTPMLITQ  
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLPPQDP  
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELG LFGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAA  
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT  
LSQSYQYEVCLAGSGTNEFKFLKPIIPNFPPQCPGKEIQGNSTFPNNFGFNIQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 685-712

#### **Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

#### **N-glycosylation site.**

amino acids 418-421, 436-439, 567-570 and 786-789



## FIGURE 164

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC  
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT  
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTG  
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG  
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC  
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG  
TGATTCTTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT  
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG  
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGCGGGAATCTGACG  
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG  
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT  
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT  
GCCGCTTTTCTGCCAGTTTGGCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT  
CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC  
TGTTCCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATAACAGATC  
GAACACTGGAAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT  
GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA  
CTGGTTGCTTGTATTTTCCTTATTCTTTTTAATTAGTTTTATTATGTATGCTACCATTCGAA  
CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA  
CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA  
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC  
AAAAATATTCATAG

## **FIGURE 165**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333

><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRPPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE  
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTTCGAGGAEDSRC  
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE  
NFTLKILNMSQDLMDFLNPNNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS  
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETCLKIFIFNQTGIEAKKNVVVTQADQ  
IGPLPSTLIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domain:**

amino acids 321-340

#### **Homologous region to dilsufide isomerase**

amino acids 212-302

#### **N-glycosylation site.**

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296

#### **Thioredoxin domain**

amino acids 211-227

## FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT  
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCCTC  
TTTGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGACAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG  
CCTTCGGCTTCCCCCTGGCCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG  
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG  
ATTTTGCACTGAAAAATAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC  
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGACAGTGACCTGTGAGGAGATGAACGACATCAACG  
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG  
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA  
GTCCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC  
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT  
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCCTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTTACCTAAAGGAAAAGCCCACCCGAATCTTGTAGAAATATTCAAACATAA  
AAATCATGAATATTTTAA

## **FIGURE 167**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSARGLFLFGQPDFS YKRSNCKPIPVNLQLCHGIEYQNMRLPN  
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQPCHSLCVQVKDR  
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM  
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSEKDLKKSVLWLKDSLQCTCE  
EMNDINAPYLVMGQKQGELVITSVKRWQKGQREFKRISRIRKLQC

**Important features:**

**Signal peptide:**

amino acids 1-20

**Cysteine rich domain, homologous to frizzled N terminus**

amino acids 6-153

109707"44532660

## FIGURE 168

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTTGCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG  
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG  
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT  
TGTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTGCAACCTCTGGGCGTCCTTGTGGCCAATGTGCT  
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATAACCATCC  
CTGCTGGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCTG  
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTGGATGGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC  
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTA  
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA  
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCCTTG  
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG  
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCCAGCACGGCGACTCCGGA  
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGGAGCCCCCACCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

## **FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN  
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPVLV  
KKGEDIPMLGVYTI PAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCLFSLACVPFALVSQLOGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV  
GEGAATGMIFVLGQAEGILIMLAMTALT VRRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF  
SCILAVFFHTPYRRLQAESGEPSPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

### **Important features:**

#### **Signal peptide:**

amino acids 1-44

#### **Transmembrane domains:**

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,  
280-300, 318-337, 341-357, 375-387, 420-441

#### **N-glycosylation site.**

amino acids 40-43 and 43-46

#### **Glycosaminoglycan attachment site.**

amino acids 468-471

# FIGURE 170

GTCCACATCCTGCTCAACTGGGTGAGTCCCTCTTAGACCAGCTCTTGCTCCATCATTGCTGAAGTGGACCAAC  
TAGTTCCCCAGTAGGGGGTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA  
TGGCCTTGCTTGGGGTCTGCTGTTTTCATAATCATCTAACTATGGGACAAGTTGTGCCGGCAGCTCTGGGGG  
AAGGAGCACGGGGTGTATCAAGCCATCCAGGAAACTGAGGAGCTTGTCCAGCCTTGAAAGAACTCTAGTGGTT  
TCTGAATCTAGCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG  
CTACTTATTTCTTTTAGGGGATTGTGAGGAGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC  
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAAGTGGGCCGGGAGGAGAGGCGGAGGCAAGCTGGGGCCGCCTT  
CCAGGTGTTGCAGCTGCCTCAGGCGCTCCCAATTGAGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCG  
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGGTTTCTTTGATGTGCTTGCCACAGGGGATT  
GGCTCTGATCCATGTGGAGATCCAAGTGTGAGCATCAATGACCACAGCCACGGTTTCCCAAAGGCGAGCAGGA  
GCTGGAAATCTCTGAGAGCGCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCCC  
TAACACCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTTGCCTTGATGTGCTTGTGGGCCCTGATGAGAC  
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAAATCCATTCAATTTTTGATCTGGTGTAACTGC  
CTATGACAATGGGAACCCCCCAAGTCAAGTACCAGCTTGGTCAAGGTCAACGTCTTGACTCCAATGACAATAG  
CCCTGCGTTTGTGAGAGTTCACTGGCACTGGAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAAAT  
GACCGCCACAGACCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCTCCAGAGGT  
GCTGGACACCTTCACTATTGATGCCAAGACAGGCCAGGTCACTTCTGCGTGCACCTCTAGACTATGAAAAGAACCC  
TGCCTACGAGGTGGATGTTGAGGCAAGGACCTGGGTCCCAATCCTATCCAGCCCATGCAAAGTTCTCATCAA  
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCAGTCAATGAGGCGCTCCAGCCATCACTGGTGTGAGAAGC  
TCTTCCCAAGGACAGTTTATTTGCTCTTGTCTATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG  
CTGGCTGAGCCAAGAGCTGGGCCACTTCAAGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCAATGC  
CACACTGGACAGAGAGCAGTGGCCCAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGGCCCTTATC  
AGCCAAGAAACAGCTCAGCATTCAGATCAGTGACATCAACGACAATGCACCTGTGTTTGAGAAAAGCAGGTATGA  
AGTCTCCACGCGGGAAAACAACCTTACCTCTCTTCACTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT  
TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCAAGTGTCTCACTTAGTAGCTATTGACTCCAACACAGGAGA  
GGTCACTGCTCAGAGGTCACTGAACATATGAAGAGATGGCCGGCTTTGAGTTCAGGTGATCGCAGAGGACAGCGG  
GCAACCCATGCTTGATCCAGTGTCTCTGTGTGGGTGAGCCTCTTGATGCCAATGATAATGCCCCAGAGGTGGT  
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCC  
CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT  
CCTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGCAAATGGAGAGCCCTCTACAGCATCCGCAATGG  
AAATGAAGCCCACCTCTTCACTCTCAACCTCATACGGGGCAGCTGTTGCTCAATGTACCAATGCCAGCAGCCT  
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT  
GAGGTCATGTTTGTCAACAGTGTGGACCACTGAGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGCTG  
GCTGACGGTGATCTGCTGGCTGACTGTTGGGCATCTTGGGTTGATCCTGGCTTTGTTTCAATGCTGCTGCCG  
GACAGAAAAGAAGGACAACAGGGCCTACAACGTGCGGGAGGCCGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC  
CCAGAAACACATTGAGAAGGCAGACATCCACCTCGTGCCTGTGCTCAGGGGTGAGGAGGTGAGCCTTGTGAAGT  
CGGGCAGTCCCACAAAGATGTGGACAAGGAGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCCCTT  
CCACCTCACCCGACCCTGTACAGGACGCTGCGTAATCAAGGCAACAGGGAGCACCGGCGGAGAGCCGAGAGGT  
CTGCAAGACAGCGTCACTTCTTCAACCATCCAGGACGGAATGCCTCCCGGAGAACCTGAACTTCC  
CGAGCCCCAGCCTGCCACAGGCCAGCCAGCTTCCAGCCCTCTGAAGGTTGAGGAGCCCCACAGGGAGGCTGGC  
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACCAGCCTCCTCTGCAACCTGAGACGGCAGCGACATCT  
CAATGGCAAAGTGTCCCCTGAGAAAGATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC  
TGCCTTCCCGAGCGGAACCCCTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTTCAAGAACTCTCCAGCTGCT  
GTCCTTGTGCTCAGGGCCAAATCCAGCCCAAACCAACACCGAGGAAATAAGTACTTGGCCAAGCCAGGAGG  
CAGCAGGAGTGCAATCCAGACACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA  
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC  
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCTCAC  
CACCAACTACCGTGACAATGTGATCTCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCCG  
CAAGGCAGAGGCACCAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGTCACT  
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCGTGGAGGCCGCTCCGAGGCGCTGCGGCGGCTCTCGGT  
CTGCGGGAGGACCCCTCAGTTTAGACTTGGCCACCAGTGACGCTCAGGCATGAAAGTGCAAGGGACCCAGGTGG  
AAAGACGGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGGCTGCTGTAACATACTCAGACGCCT  
CTGGATCCAAGAACCAGGGGCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACTCACTAGCTAG  
CGGCGGCTGAGAACTTTAGGGTGACTGATGCTACCCCAACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC  
TGACCAAAGCAGCCCCCTTGTAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGT  
TCCTGGCAAACATATGTGGAGCACAAAGGTCAGTCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG  
AAAGGGTGGCCTTCTTGGGTAGCAGGAGTCAAGGGGCTGTACCTGGGGGTGCCAGGAAATGCTCTCTGACCTAT  
CAATAAAGGAAAAGCAGTAAAAA

FIGURE 170

## **FIGURE 171**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331

<subunit 1 of 1, 1184 aa, 1 stop

<MW: 129022, pI: 5.20, NX(S/T): 5

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTKYQVSEEVPSGTVIGKLSQELGREERRRQA  
GAAFQVLQLPQALPIQVDSEGLLSTGRRDLREQLCRQWDPCLVSFVLDLATGDLALIHVEIQ  
VLDINDHQPRFPKGQELEISEASLRTRIPLDRALDPDTGPNLHTYTLSPSEHFALDVIV  
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPFAESS  
LALEIQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDNDNIPSIHVTWASQPSLVSEALPKDSF  
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD  
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHADLGINGKVS  
YRIQDSPVAHLVAIDSNTGEVTAQRSLNYYEEMAGFEFQVIAEDSGQPMLASSVSVVWSLLDA  
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLLT  
IVARDADSGANGEPLYSIKNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS  
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK  
KDNRAYNCREAESTYRQQPKRPQKHQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA  
GWDPCLOAPFHLTPTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLLNLEP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEGGS  
RSAIPDTDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL  
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAAAGMKVQGDGPGKGTGTEGKSRGSS  
SSSRCL

**Important features:**

**Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 719-739

**N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

**Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563



## FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT  
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTTACATTGGC  
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACACGACTGCTTTTTTCTGTCTCTT  
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTTCTCAGCCCCA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGA CTCTC  
ATGGCTCTTCTTTCTGGATTGGTGTCTCAACTGCCCATACACTTACATGTCTTACTTCTT  
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA  
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA  
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTACCACCTCAGCATCAGG  
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC  
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC  
AAGGGGAAATATTTTAAATTTTCTTGGTTACTTTTTCTCTATTTTACTGTGTTTGGAAAATTTT  
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCACAAGAGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT  
TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTTCCAATGTCAATTGTCTGCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA  
TACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT  
TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC  
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTTAAGCCTACTACAGACTGTTAGAGGCCAGT  
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC  
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCCGTCAGGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA  
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA  
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT  
AGGATTTCCGTTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT  
AAAATCAGAGACTGTAAACAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

## **FIGURE 173**

MSFLIDSSIMITSQILFFFGWLFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEI  
LGVLNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTIFYFF  
WKLGDPPILSPKHGILSIEQLISRVGIVGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ  
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS  
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160



## **FIGURE 175**

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC  
TTTNTTGAATTCGGGTTNNGNATACCTTCCAGAAAATATTTTTTGGATTTGGGGTAGNTT  
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTTCATGGTGCCTTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTTCCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN  
TAGGAGATCCCTTTCCCATTC

09544-101-4582660

[illegible]

## FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL  
GVSVRSQGPQGGKIVTCAHRYEARQQRVDQILETRDMIGRCFVLSQDLAIRDELGGGEWKFCG  
RPQGHQFQFGCQQGTAAAFSPDSHYLLFGAPGTYNWKGRTARVELCAQGSADLAHLDDGPYEA  
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSGFGYSLAVADLNSDGWPDLLIVGAPYFFERQEELGGAVYVYLNQGGHWAGI  
SPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAGAPFDGDGKVFYIHGSSLGVVAKPSQVLE  
GEAVGIKSFYSLSGSLDMDGNQYPDLLVGSADTAVLFRARPILHVSHEVSIAPRSIDLEQ  
PNCAGGHSVCVDLRVCFYSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEPK  
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTPRLRRQAPGQGLPPVAP  
ILNAHQPSQRAEIHFLKQCGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA  
LSGQPVIGLELMVTNLPSPDPAQPQADGDDAHEAQLVLMPLPDSLHYSVGRALDPAEKPLCLSN  
ENASHVECELGNPMKRGAQVTFYLLSTSGISIEETTELEVELLLATISEQELHPVSARARVF  
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVYEVTVSNQGSRLTLGSAFLNIM  
WPHEIANGKWLLYPMQVELEGGQGPQKGLCSRPNIHLHDVDSRDRRRRELEPPEQQEPGE  
RQEPSMSWWPVSSAEKKKNITLDCARGTANCVVFSCLYSEFDRAAVLHVWGRWNSTFLEEY  
SAVKSLEIVIVRANITVKSSIKNLMLRDASTVIPVMVYLDPMVVAEGVPWWVILLAVLAGLL  
VLALLVLLLLWKMGFFKRAKHPEATVPQYHAVKI PREDRQQFKEEKTGTILRNNWGSPPREGP  
DAHPIAADGHPDELGPDGHPGPGTA

### **Important features:**

#### **Signal peptide:**

amino acids 1-33

#### **Transmembrane domain:**

amino acids 1040-1062

#### **N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

#### **Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-  
407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408  
and 1031-1047

## FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACAACAAGATGCTCAAGGTGTCAGCCGTA CTGTGTGTGTGTCAGCCGCTTGGTGCAGTCA  
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC  
TGGATGATAAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCTTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC  
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGA  
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAAACTATGACCT  
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG  
CATTCCTTCAATTCTTGTGACACATAACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC  
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA  
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACACAATGTCATGGCAGTGTTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT  
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC  
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTA  
CAAAAATGATAGCCTATTTAAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT  
AAGAATCATTTGCTTTGAGTTTTTATATTCTTACACAAAAAGAAAATACATATGCAGTCTA  
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTTACGAGAACAACTTTGT  
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG  
ATAATTCTAAGTGAAATTTAAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAAAA

## **FIGURE 179**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA  
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP  
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKTKTLLRPERSRFDTSILPI  
CKDSLGMFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ  
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSVGQCWCVDRYGNEVMGS  
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDEDEDEGDDDDGGDDHDVYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Leucine zipper pattern.**

amino acids 246-267

#### **N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

#### **Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352





## **FIGURE 181**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFLLPAGQKECFYQPMPLKASLEIEY  
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFEL  
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN  
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 195-217

#### **N-myristoylation site.**

amino acids 43-48

#### **Tyrosine kinase phosphorylation site.**

amino acids 55-62

## **FIGURE 182**

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATAACCAGAT  
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCCTGGATG  
CTGCTTTCCTGCCTCATTCTCCTGTGTCAAGGTGAAGAAACCCAGAAGGAACTGCC  
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCCTGGTGAGGAGCATTAG  
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC  
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCC  
TTCTTTTTCTTTTTCTTCACCTTCATTTCAAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

109707 44582660

## FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM

DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS

TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

**Important features:**

**Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

097544-10103

**SECRET**

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTCTGGC  
TGCTTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCACACAGGAGTGT  
CGGACTGTGTACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCGTGTCTGTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGGCCCTCACGCTC  
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

## FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP

FQGDSTVTKSCASKCKPSDVGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

095844582660

## FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG  
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC  
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTTGAAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC  
TTGCCGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA  
GACACTAAACCAGCTATCCAAATGCAGTGAATCCTTTTATATAATAGATGCTATGAAAACC  
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT  
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTG  
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA  
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT  
TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA  
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAA

## **FIGURE 187**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA  
APGILYPGGNKYQTIIDNYQPYPCAEDDEECGTDEYCASPTRGGDAGVQICLACRKRKRCMRH  
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG  
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ  
KDHHQASNSSRLHTCQRH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 256-259

#### **Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126



## **FIGURE 188**

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG  
GAGTCCTTNTGAGANGATGGTTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC  
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT  
TGCAGTCAGCGCCGCGCCGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCCGGAATTACTGCAAAAATGGAATATGTGTGTNTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGG

44584660

## FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGC GCCCGCGG  
 CTGGGCCGTCGGAGAGTGCCTGTGCTTCTCTCTGCAACGCGGTGCTTGGGCTCGGCCAGGCGGGTCCGCCGCCA  
 GGGTTTGGAGTGGGGAGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTTGTGGAAATGAAAAGGA  
 AGTATTAGAAATGAGCTGAAGACCATTACAGATTAAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCCT  
 TGAAGTAATGTAGACAGAAGTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC  
 TTAATCAGAACTTGCATAAGAAAGAGAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG  
 GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTGG  
 AGTGTCCAAAAC TGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA  
 AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA  
 TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA  
 CTATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC  
 TGCTGTTAATTTCTGGAGAACTGTGGTTTGTAAATTTTTACTCCCCAGGCTGTTTCACTGCCATGATTTAGCTCC  
 CACATGGAGAGACTTTGCTAAAGAAAGTGGATGGGTACTTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAA  
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCCAGTCTCTTCAATTTTTCGGTCTGGAATGGCCCCAGTGAAATA  
 TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG  
 GACAGGAAATTTTGTCAACTCCATACAACTGCTTTTGTCTGCTGGTATTGGCTGGCTGATCACTTTTTTGTTCAAA  
 AGGAGGAGATTGTTTGACTTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTTGGATGCTAA  
 AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAAGTACTTTCCGCAACACACTAGAGGATCGTTT  
 GGCTCATCATCGGTGGCTGTTATTTTTTCAATTTTGGAAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAAACT  
 AAAAATCTACTTTAAAAATGATCATATTTCAAGTTGGCAGGTTTGAAGTCTCTGACCCAGACATCTGTAGTAA  
 TCTGTATGTTTTTCAAGCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGAAATTCATCATGGAAA  
 GAAGATTTCTATATGATATACTTTGCCTTTGCCAAAGAAAGTGTGAATTTCTCATGTTACCACGCTTTGGACCTCAA  
 TTTTCTGCCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCCCTGGTGTCCACCATGTCGAGCTTTACT  
 ACCAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTATGA  
 GGGACTCTGTAAACATGTATAACATTCAGGCTTATCCAACAACAGTGGTATTCAACAGTCCAACATTCATGAGTA  
 TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC  
 ACCCACCACCTTCAACGAAGTAGTTACACAAAGAAAAACAACGAAGTCTGGATGGTTGATTTCTATTTCCGTTG  
 GTGTCATCCTTGGCCAAGTCTTAATGCGCAAGATGGAAAAGAAATGGCCCGGACATTAACTGGACTGATCAACGTTGG  
 CAGTATAGATTGCCAACAGTATCATTTCTTTTTGTGCCCGAGAAAACGTTCAAAGATACCTTGAGATAAGATTTTT  
 TCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATTTCCCTGAGAAT  
 CTGGGGTCTAGGATTTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTTCAAGTAAAAAGTTCTACAAGG  
 GAAAAATCATTTGGGTGATTTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGTCTCCAGAATTTGAGCT  
 CTTGGCTAGGATGATTAAGGAAAAAGTGAAGCTGGAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAG  
 AGCTGGGATCAGGGCCTATCCAAGTGTAAAGTTTATTTCTACGAAAGAGCAAGAGAAATTTTCAAGAGAGCA  
 GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAAAATTGGAAACTCTCCGAAATCAAGGCAA  
 GAGGAATAAGGATGAACCTTGATAATGTTGAAGATGAAGAAAAAGTTTAAAGAAATTTCTGACAGATGACATCAG  
 AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA  
 GAATTTATCTACAGCACTGGTGTAAAGAAAGGCTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTTATAAATATTTTA  
 GACTTTTGAGGCTATAATATATGGTTTACACATGAGAACAAGAATAGAGTCATCATGTATTCTTTGTTATTTGCT  
 TTTAAACAACCTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCAAGTCCATG  
 GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT  
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTTCAGTTTTTTGGCTGACCTGAAAAGAGGTAAC  
 TAGTTTTTGGTCACTTGTCTCTCTAAATAATGCTATCCCTAACCATATATTTATATTTCTGTTTTTAAACACCCAT  
 GATGTGGCACAGTAAACAAACCTGTTATGCTGTATTATTAGAGGAGATTCTTCATTGTTTTCTTTCTTCTCA  
 AAGGTTGAAAAATGCTTTTAAATTTTTCACAGCCGAGAAACAGTGCAGCATATATGTGCACAGTAAGTACAC  
 AAATTTGAGCAACAGTAAGTGACAAATTTCTGTAGTTTGTGCTGATCATCCAGGAAAACCTGAGGGAAAAAATTA  
 TAGCAATTAAGTGGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA  
 TGTGTTTATGATTTTCTGAAATGCTTTTATAGAAATTTTCCACTGATAGTTGATTTTTGAGGCATCTAATAT  
 TTACATATTTGCTTCTGAACTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTTTTCTTTTATAGTTTTGG  
 TTTTTCACTCCTGTCCAGTCTATTTATTTTCAAATAGGAAAAATTACTTTACAGGTTGTTTTTACTGTAGCTTAT  
 AATGATACGTAGTTATTTCCAGTTACTAGTTTACTGTGAGGGCTGCCTTTTTTCAAGATAAATATTGACATAATA  
 ACTGAAGTTATTTTTATAAGAAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTTCTGTGTTGTTTGA  
 CTCAAAGAAATCACAAATTTGTGAGTAACATGTAGTTGTTTGTAGTTATAAATTCAGAGTGTACAGAATGGTAAAAAT  
 CCAATCAGTCAAAGAGGTCATGAATTAAGAGGCTTGCAACTTTTTTCAAAAAA

10907-44532660

## FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL  
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYRYDFGI  
YDDDPEIITLERREFDAAVNSGELWVFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRMLCRMKGVNSYPSLFI FRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS  
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN  
TLEDRLAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP  
SLAVFKGQGTKEYEIIHGGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS  
AEQILEFIEDLMNPSVVSILTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG  
FLPQVSTDLTPTQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPPEFELLARMIKGKVKAGKVDC  
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGKRNKDEL

### **Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

## FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA  
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGGA  
GTCGTTGGTGAAGTTTTTCATTCCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCCTTACCTCATCCCATAT  
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT  
GGGAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCACCA  
AAAATCCAAGCACAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA  
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTCTGAG  
ACTACAGAAGTTTCTTCCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT  
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATTGAAATAAATAAGCTCCAGCCAGAGATG  
TATGCATGATAATGATATGAATAGTTTTCGAATCAATGCTGCAAAGCTTTATTTACATTTTTT  
TCAGTCCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCTTCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCTT  
TCATGCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT  
TTTATTTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT  
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTAAGATTGAGCATTGAAAGATTTCCCTAGCCTCTTCCTTTT  
TCATTAGCCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT  
AACTCTGAAGTCCACCAAAAGTGGACCCTCTATATTTCCCTCCCTTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA  
TAACCTTTTTCTTTGTAATTTATGCTTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT  
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA  
CAATGGACCCAAGAGAAGAA

09978544.101601

## **FIGURE 192**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI  
LVLWDINKRGVEETAAECKRLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV  
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC  
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFNVTGFTKNPSTRLWPVLETDEVVRSLID  
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

#### **Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219

TO9TOT"44582660

## FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCAGCAGG  
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGAGAGGGCCCAGCCCCCGGGGCG  
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCT  
GCTGATCATCGTGACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT  
CTAGGCCGCACACGGGGCCGCCGCTGCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACG  
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGACGACCGGCACGGGG  
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA  
CGTGCAACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT  
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTTCTTCTGTCGCGACCCC  
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCCGCTCGGCGC  
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA  
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC  
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC  
GAGACTGAAGCTTTCGCGTTGCTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCC  
AGTTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

## **FIGURE 194**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSVFMILLIIVYWDSAGAAHFYLHTSF SRPHTGPPLPTPGPDRDRELT  
DSDVDEFLLDKFLSAGVKQSDLP RKETE QPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER  
RSVLRGFCANSSLAFFPTKERA FDDIPNSEL SHLIVDDRHGAIYCYVPKVACTNWK RVMIVLS  
GSL LHRGAPYRDPLRIPREHVHNASAH LTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF  
VRLISAFRSKFELNEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLD EDAQLLQLLQVDRQLRFPPSYRNRT  
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLF GYPK PENLLRD

### **Important features:**

#### **Signal peptide:**

amino acids 1-31

#### **N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

#### **TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

TOGETHER

## **FIGURE 195**

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACAGCGGGGCCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC  
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC  
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA  
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG  
CCTACTGGGCCCGCATGGGCCAGCCCGCTGAGGTGGGGCTGCGGCAGTGTTCCCTGGCCTCCGA  
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGACAGAGCTGGGGTACGGGT  
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCCTTGATTTCTCTCATTT  
CTACTTGGGGCCCCCTTCCTAGGACTCTCCCACCCCAAACCTCCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT  
AAAAACGATTTGCAGCC

097544-1001  
T02T01-1458/66



## **FIGURE 196**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD  
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPPQRPEETSAQGFRQLLELNLLGTYTLTKL  
ALPYLRKSQGNVINISLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN  
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTTGG  
AELGYGCKASRSTPVDAPDIPS

**Important features:**

**N-glycosylation site.**

amino acids 138-141

**Short-chain alcohol dehydrogenase family protein**

amino acids 10-22, 81-91, 134-171 and 176-185

209607 44582660

## **FIGURE 197**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGA CTGGCCTCACAACCTG  
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC  
TGGTGTACGGATGAAACCGTATGCCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCCTGTGTCTGGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCCAGCCAGGTTCCTGTGCGCCGCCG  
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA  
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG

FIGURE 197

## **FIGURE 198**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRIIPVDLPEARCLCL  
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

0997544 10101  
T09T0T" 44532560

## FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG  
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG  
GCGCCCAACATGGCGGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGAT  
CGCGGCTGTGGCGGCGACGGCAGGCCCGGAGGAGCGCGCTGCCGCCGGAGCAGAGCCGGG  
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT  
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTGAGAATGGGAGGCTTTTGCAAAGAA  
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCAATCAAGAACCAGGTTTGAGTG  
GCCGCTTCTTTGTCACTACTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGT  
TATCGTGGCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC  
AGTCGAGCCTCTGACTGGCTGGAAATCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC  
TTTTTAGCATCTCTGGCAAGATATGGCATCTTACAACTATTTACAGTGACTCTTGGAATT  
CCTGCTTGGTGTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGG  
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC  
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG  
GAGGAAAAAGATGATTCAAATGAAGAAGAAAAACAAAGACAGCCTTGATAGATGATGAAGAAGA  
GAAAGAAGATCTTGCGGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTG  
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG  
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC  
TGACACAGAGGTGGTGGAAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC  
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTGAGCTTCCCTTTGG  
CCTGCAGTTTGTACCAAATCCTTAATTTTTCTGAATGAGCAAGCTTCTCTTAAAAGATGCT  
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT  
GACAATCAGGATATAGAAAAACAAACGTAGTGTTGGGATCTGTTTGGAGACTGGGATGGGAA  
CAAGTTCAATTTACTTAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCAGTCCTAATC  
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT  
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGATCCTTTTTCTTGTGTAAAGTATTTAT  
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA  
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG  
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTGAGGCTCT  
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC  
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT  
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT  
TTACAAGACAGATTAAAAAAAATTTGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTT  
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCTCTAAGTCTTGCCAGTACAAGGTAGT  
CTTGTTGAAGAAAAGTTGAATACTGTTTTGTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC  
TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCTTCAGTGATGTGCTTTTGGTGAAA  
GAATTAATGAACCTCAGTACCTGAAAGTGAAAGATTGATTTTGTTCATCTTCTGTAAATC  
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG  
GCTAATTTCTTT

09978544-101601

## FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP  
WCPSCQQTDSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG  
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSE RSEQNRRSEEAHRAEQLQDAEEEEK  
DDSNEEENKDSLVDDEEEKEDLGDEDEAE EEEEEEDNLAAGVDEERSEANDQGPPGEDGV TRE  
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Transmembrane domain:**

amino acids 191-211

#### **N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

#### **Flavodoxin proteins**

amino acids 173-187

## FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTAACTCCGGTAAGTACCTAGCCCACATGATT  
 TGAATCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC  
 CAAATGCTATATCTATTCAAGGGGCTCTCAAGAACAATGGGAATATCATCCTGATTTAGAAAAT  
 TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT  
 TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG  
 GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTCTTTTCC  
 AGCCCTTGTCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTCAAGCATGTCACT  
 AAATTCCTGGGATGGAAGTAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG  
 ACAGCTCAAATGAATTGGGATTTATAGTAAACAAGTGTCTTCCCAACCTGATAATTCATTT  
 TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT  
 CTCTTCTAACTTATTTTCAAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG  
 TATGGATTACAGTGTCACTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT  
 GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA  
 AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG  
 TTTAGAGAGCTTGGCCAACTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT  
 GTATTTGTGACCTACAGGTAGGCTAGTATTATTTTCTAGTTAGTAGATCCCTAGACATGG  
 AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTTATTTTGTAGATAGGGTCT  
 CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC  
 CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG  
 TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG  
 TGATCTGCCCCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC  
 CCCAAGCTTGAATTTTCAATCTGCCATTGACTTGGCATTACCTTGGGTAAGCCATAAGCGA  
 ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT  
 GTGTTGCCACGATTTGACCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAT  
 ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT  
 ATTATTTTCTCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAATCCTA  
 CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT  
 TTTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTCGCTCTTGTGCCCAGGCTGGAGTGCACGG  
 CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT  
 CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGT  
 AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC  
 CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT  
 TGTATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA  
 AAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA  
 ACAAGTATTAACATTTTGAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT  
 ACCATTTTTTTTCAAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG  
 TGCTGATTTGTCTTATTTTTTTTCACTTTTCCACTGGTGCTATTTTTTATTTCCAATGGATA  
 TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAAATATGTGAAAAGAAAT  
 TGTACCAATTTTACTAAATTATGCAGTTTAAATGGATGATTTTATGTTATGTGGATTTTCA  
 TTCAATAAAAAAAACTCTTATCAAAAAA

T09T0T"445B2660

## **FIGURE 202**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

**Important features:**

**Type II transmembrane domain:**

amino acids 45-65

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

**N-myristoylation sites.**

amino acids 35-40 and 151-156

**Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

09544-1000





## **FIGURE 204**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE  
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH  
QEESLAQGPPLLATSVTSWWSPQNI SLPSAASF TFSFHSPHTAAHNASVDMCELKRDLQLL  
SQFLKHPQKASRRPSAAPASQQQLQSLESKLT SVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVD FSSQALFQDKNSSQVLGE  
KVLGIVVQNTKVANL TEPVVLTFQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGCETVRRE  
TQTSCFCNHLTYFAVLMVSSVEVD AVHKHYLSLLSYVGC VVSALACLVTIAAYLCSRVP LPC  
RRKPRDYTIKVH MNLLLA VFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE  
GYNLYRLVVEVF GTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPI ILAVHRTPEGVIY  
PSMCWIRDSLVS YITNLGLFSLVFLFN MAMLATMVVQILRLRPHTQKWSHVL TLLGLSLVLG  
LPWALIFFSFASGTFQLVVLYLFSIITSFQGF LIFIWYWSMRLQARGGPSPLKSN SDSARLP  
ISSGSTSSSRI

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Putative transmembrane domains:**

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

#### **Microbodies C-terminal targeting signal.**

amino acids 691-693

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

#### **N-glycosylation sites.**

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

#### **G-protein coupled receptors family 2 proteins**

amino acids 475-504

## **FIGURE 205**

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA  
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACCTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT  
GGTGTTTCTGTTCAACATGG

09978544-101601

## FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCCAGGTTTTGCTTTGA  
TCCTTTTCAAAAACCTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCT  
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCCAAGTGCAGCCTTCCCTGGCGGTGGTGAAGAGAC  
TCGGGAGTCGCTGCTTCCAAAGTGCCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGC  
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC  
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG  
GAAGTATTCACAGCCCAAGGTTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG  
AGGAAAATGTATGGATACAACCTTACGTTTGTATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
ATGATTTTGTAGAAGTTGAGGAACCCAGTGTATGGAACCTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG  
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAGGGT  
TCTGTCATCCACTACAACATTGTCTATGCCACAATTACAGAAAGCTGTGAGTCTTTCAGTGCTACCCCCCTTCAGCTT  
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGACCTTATTTCGATATCTTGAACCAG  
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTTGGAA  
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCT  
CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCAATTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG  
GTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC  
ACGAGGTCTTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTACCGACGTGGCCCTGGAGC  
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA  
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACCTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTTGCT  
TCAAGGACCTTTTATCTTCAGGATTTACAGTGCAATTTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA  
ACAGCTCTTTTGGAGAGGAGGCTTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTAT  
TAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTC  
GATACGGCTTAGGGTAATGTCTAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC  
TCTAAAGCTCCATGTCTGGGCCATAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTCACAT  
ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAACTTGT  
GTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATAATTTCTGCCATTTAGAAGAAGAGAACTACA  
TTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG  
TTTCATTGTGTACATTTTTATATTTCTCTTTTGGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT  
ATTTTTTACCAAAGGTATTTAATATTTCTTTTTTATGACAACTTAGATCAACTATTTTTTAGCTTGGTAAATTTTTCT  
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA  
TTCTCGTATGGTGTCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA  
GACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA  
AAGTAGACATTCAGATCCAGCCATTACTAACCTATTTCCTTTTTTGGGAAATCTGAGCCTAGCTCAGAAAAACAT  
AAAGCACCTTGAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCTATTTA  
TTGTGATGTTGTGGTTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTATGTACA  
GAAGTATGCTCTTAAACAGTTCACTTATTGTACTCTGGCAATTTAAAAAGAAAATCAGTAAAATATTTTGCTTGT  
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAGA  
ATGTGGCTATTTTGGGAGAAAAATTAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCCAGGTTTTGCTTTGA

## FIGURE 207

MSLFGLLLLT SALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAVEENVWQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC  
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL  
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLEEVRLY  
SCTPRNFSVSIREELKRDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQ  
LRPKTGVRGLHKSLTDVALEHHEECDVCVCRGSTGG

**Signal sequence:**

amino acids 1-14

09584660

# FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGAAGA  
 AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATCTTATCCTTTTAAACATAATCCTAATTTCC  
 AAACCTCCTTGGGGCTAGATGGTTTCTTAAACTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG  
 ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATTTCCACGAACACCACGAACCTCACCTC  
 ACCATTAACCACATACCAGACATCTCCCCAGCGTCTTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCAGA  
 TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC  
 TTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATACCGCAGGGCCTCCCG  
 CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC  
 AACATAGAAATACTCTACCTGGGCCAAAACCTGTTATTATCGAAATCCTTGTATGTTTCAATTCAATAGAGAAA  
 GATGCCTTCTTAAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCCTACTGTT  
 TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC  
 CTCAACCAATTACAAATTTCTTGACCTAAGTGGAAATGCCCCGTGTTTATAATGCCCCATTTCTTGTGCGCCG  
 TGTAATAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGCAGAGATTAAAAGTTTTACGTCTA  
 CACAGTAACCTCTCTTACAGATGTGCCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACCTGGATCTGTCC  
 CAAAACCTTCTTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCAATTGGATCTG  
 TCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG  
 AAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA  
 AATCTTGAAGTTCTTGATCTTGGCACTAACTTTTAAAAAATGTAACTCAGCATGTTTAAACAATTTAAAAGA  
 CTGAAAGTCATAGATCTTTCACTGAATAAAATATCACTTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT  
 GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCTTGAACAATTACATTATTTAGATATGATAAGTATGCA  
 AGGAGTTGCAGATTTCAAAAACAAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC  
 TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTTCAGCATCTTTCTTTCTCAAATGCCTC  
 AATCTGTGAGGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATCCAACCTTTAGCAGAGCTGAGATATTTG  
 GACTTCTCCAACAACCGGCTTGATTTACTCCATTTCAACAGCATTTGAAGAGCTTCACAAAGTGAAGTTCTGGAT  
 ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTAATCATATGCTAAACTTTACCAAGAACCTAAAGGTT  
 CTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA  
 ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG  
 AATCTGCTAAAATTAGAGGAATTAGACATCTCTAAAAATTCCTAAGTTTCTTGCCTTCTGGAGTTTGTGATGGT  
 ATGCCTCCAAATCTAAAGAATCTCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT  
 CTAAAGAACCTGGAACCTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAGAGATTATCCAAGTGTTC  
 AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC  
 CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTC  
 AACAATCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG  
 GTTAACCATACGGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC  
 CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA  
 TCTGTATCTCTCTTTCTCATGGTGATGATGACAGCAAGTCACTCTATTTCTGGGATGTGTGGTATATTTACCAT  
 TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT  
 GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAAGAGAGAAA  
 CATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCAGAGCATA  
 CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAAGACTGAAAATTTTAAGATAGCATTTTAC  
 TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTTCAGAAG  
 TCCAAGTTCTCCAGCTCCGGAAAAGGCTCTGTGGGAGTTCTGTCTTGTGAGTGGCCAACAAACCCGCAAGCTCAC  
 CCATACCTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA  
 ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

109101 44582660

## **FIGURE 209**

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG  
IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGNQNCYR  
NPCYVSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL  
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF  
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLSKSL  
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDTGTNFIKIANLSMFKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ  
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH  
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMDNDISSSTSRTMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSLFLPSGVFDGMPPNLKNLSL  
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ  
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHNRFLCTCDVWFVWWVNHTVETIP  
YLATDVTCVGPGAHKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLCLEE  
RDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 840-860

## FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAACAGAAACATGGAACATGTTCTTTC  
AGTCGTCAATGCTGACCTGCATTTTCTGCTAATATCTGGTTCCTGTGAGTTATGCGCCGAAGAAAAATTTTCTA  
GAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGCGAGAGTGCAGCAATCGTCGACTACAGGAAG  
TTCCCCAAACGGTGGGCAAATATGTGACAGAACTAGACCTGTCTGATAATTTTCATCACACACATAACGAATGAAT  
CATTTCAGGGCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACCGAAATC  
CCGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCTCAACCTAAAAAACCTAAGGGAGTTACTGC  
TTGAAGACAACACAGTTACCCCAAATACCTCTGGTTTGCCAGAGTCTTTGACAGAACTTAGTCTAATTCAAAACA  
ATATATACAACATAACTAAAGAGGGCATTTCAGACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAAGTGT  
ATTTTAACAAAGTTTGGGAGAAAACTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT  
CACTATCTTTCAATTCTTTTCACACGTGCCACCCAACTGCCAAGCTCCCTACGCAAACTTTTCTGAGCAACA  
CCAGATCAAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTACTAGATTTAAGCGGGAAC  
GTCCGAGGTGCTTCAATGCCCCATTTCCATGCGTGCCTTGTGATGGTGGTGTCTCAATTAATATAGATCGTTTTG  
CTTTTCAAACTTGACCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGT  
TTAAAAATATGCCTCATCTGAAGGTGCTGGATCTTGAATTCACCTATTTAGTGGGAGAAATAGTCTCTGGGGCAT  
TTTTAACGATGCTGCCCCGCTTAGAAATACTTGACTTGTCTTTTAACATATATAAGGGGAGTTATCCACAGCATA  
TTAATATTTCCAGAACTTCTCTAAACTTTTGTCTCTACGGGCATTGCATTTAAGAGGTTATGTGTTCAGGAAC  
TCAGAGAAGATGATTTCCAGCCCCTGATGCAGCTTCCAACTTATCGACTATCAACTTGGGTATTAATTTTATTA  
AGCAATCGATTTCAAACCTTTTCCAAATTTCTCAATCTGGAATTTATTTACTTGTGAGAAAAAGCAATATCAC  
CGTTGGTAAAAGATACCCGGCAGAGTTATGCAAAATAGTTCTCTTTTCAACGTCATATCCGAAACGACGCTCAA  
CAGATTTTGTAGTTTGTACCCACATTCGAACCTTTTATCATTTTCAACCGTCTTTTAAATAAGCCACAATGTGCTGCTT  
ATGGAAGAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCAATGGGCCAAACCAATTTGAAAACTTCTCTGACA  
TTGCCGTGTAAATCTGTCTGCAAAATAGCAATGCTCAAGTGTAAAGTGAACCTGAATTTTCAGCCATTCCTCATG  
TCAAATATTTGGATTGACAAAAAATAGACTAGACTTTTGATAATGCTAGTGTCTTACTGAATTTGTCGACTTGG  
AAGTTCTAGATCTCAGCTATAATTCACACTATTTCAGAATAGCAGGCGTAACACATCATCTAGAATTTATTTCAA  
ATTTCAAAATCTAAAAGTTTAAACTTGAGCCACAACAACATTTTATACCTTAAACAGATAAGTATAACCTGGAAA  
GCAAGTCCCTGGTAGAATTAGTTTTAGTGGCAATCGCCTTGACATTTTGTGGAATGATGATGACAAACAGGTATA  
TCTCCATTTTCAAAGGTCTCAAGAATCTGACACGTCTGGATTTATCCCTTAAAGGCTGAAGCACATCCCAATG  
AAGCATTCCTTAATTTGCCAGCGAGTCTCACTGAACATCATATAAATGATAATATGTTAAAGTTTTTAACTGGA  
CATTACTCCAGCAGTTTCTCGTCTCGAGTTGCTTGACTTACGTGGAACAAACTACTCTTTTAACTGATAGCC  
TATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCACCTACCTCTGGCTTTC  
TTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAATCTGCTAAAAACAATCAACAAATCCGCACTTG  
AAACTAAGACCACCACCAATTTATCTATGTTGGAATACACGGAAACCCCTTTGAATGCACCTGTGACATTTGGAG  
ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTTCCAGACTGGTAGATGTCAATTTGTGCCAGTCTTG  
GGGATCAAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACCACTTGTGTTTCAGATGTCACTGCACTGATATTAT  
TTTTCTTCACGTTCTTTATCACCACCATGGTTATGTTGGCTGCCCTGGCTCACCATTTGTTTTACTGGGATGTTT  
GGTTTATATATAATGTGTGTTTAGCTAAGGTAAAAGGCTACAGGTCTCTTTCCACATCCCAAATTTCTATGATG  
CTTACATTTCTTATGACACCAAGATGCCTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACTTGAAG  
AGAGCCGAGACAAAAACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACC  
TCATGCAGAGCATCAACCAAGCAAGAAAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAGCTGGAATTTA  
AAACAGCTTTTACTTTGGCTTTGCAGAGGCTAATGGATGAGAATGAGTGTGATTATATTTATCTGCTGGAGC  
CAGTGTACAGCATTCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACA  
ACCCGAAGGCAGAAGGCTTGTTTTGGCAAACCTCTGAGAAATGTGGTCTTGACTGAAAATGATTACCGGTATAACA  
ATATGTATGTGATTCATTAAAGCAATACTAACTGACGTTAAGTCATGATTTTCGCGCCATAATAAAGATGCAAG  
GAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATTTATCCCAAACTTAGTGGTTTAAAAACAACA  
TTTGTGCTGGCCACAGTTTTTGGGGTCAAGGCTCAGGCTCAGGCTCAGCATAACTGGGTCTCTGCTCAGGGTGTCTCAG  
AGGCTGCAATGTAGGTGTTTACCAGAGACATAGGCATCACTGGGGTCACTCATGTGGTTGTTTTCTGGATTCA  
ATTCCTCTGGGCTATTGGCCAAAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCCAAGGCAGCTTGCTTC  
ATCAGAGCTAGCAAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAAATCGAATCAAAAAGTGAT  
ATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCCACTGCTCCATGGGAGTGACCACC  
TCAGTCCAGGGAAAAACAGCTGAAGACCAAGATGGTGAGCTCTGATTGCTTCAGTTGGTCATCAACTATTTTCCCT  
TGACTGCTGCTGGGATGGCCTGCTATCTTGATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACC  
ATCTTAGCAGTTGACCTAACACATCTTTTCAATATCTAAGAACCTTTTGCCACTGTGACTAATGGTCTTAATA  
TTAAGCTGTTGTTTATATTTATCATATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTTCGGTTTTAT  
TTACAGTTGCTTTTACAAATATTTGCTGTAACTTTGACTTCTAAGGTTTAGATGCCATTTAAGAACTGAGATGG  
ATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAGTATGCAGCTAAATTCGAAGCTTTTGGTCTATA  
TTGTTAATTGCCATTGCTGTAAATCTTAAATGAATGAATAAAATGTTTCATTTTACAAAAA

## FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPTVG  
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFNLN  
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV  
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL  
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNLTLQLRYLNLSSSTSLRKINAAWFKNM  
PHLKVLDFENYLVGEIVSGAFLTMLPRLEILDLSFNIIKGSYPQHINISRNFSKLLSLRAL  
HLRGYVFQELREDDFQPLMQPLNLSTINLGINFIKQIDFKLFQNFNLEIIYLSNRI SPLV  
KDTRQSYANSSSFQRHIRKRRSTDFFEDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELS DLEV  
LDLSYN SHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYT LTDKYNLESKSLVELVFSGNRL  
DILWNDDDNRYISIFKGLKNLTRLDLNRLKHIPNEAFLNLPASLTE LHINDNMLKFFNWT  
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTL LLSHNRI SHLPSGFLSEVSSLKHL DLS  
SNLLKTINKSALETKTTTKLSMLELHGPNPFECTCDIGDFRRWMDEHLNVKI PRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK  
GYRSLSTSQTIFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWD PGLAIID  
NLMQSINQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDV IIFILLEPVLQHSQYLRL  
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNMYVDSIKQY

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 826-848



## FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA  
GCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCGCCTGGAGGACACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
CTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT  
CCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCCTCA  
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA  
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA  
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGCCGG  
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA  
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC  
CCCCTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC  
TGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTG  
GAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG  
GACTGAGCCCCCTACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAG  
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC  
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG  
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG  
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTGA  
AAAGGGCGGCCGCGACTCTAGAGT  
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT



## FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG  
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC  
AGCAGCATCAGAGCAGCCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCCGCTGTGA  
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCAACGGGGGCCCCGGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG  
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTC  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC  
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA  
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCCTGTCTCCGAGTCGTTG  
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC  
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA  
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT  
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA  
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCC  
TGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG  
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT  
GGAGGAGAAGCTGCAGCTGGTGTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC  
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC  
TCCCTGAGCGAGCAGATTTCTTCTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGA  
CTCGTGACTGCCCCAGCGCTCCAGGCTGGACTGAGCCCCCTACGCCGCCCTGCAGCCCCCATG  
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC  
AGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT  
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA  
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC  
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC  
CCCCAGCACAAATAAAAATGAAACGTG

## **FIGURE 215**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

T09T0T"445B2660

## FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT  
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC  
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC  
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG  
GGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC  
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG  
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGCTAGGAGGGGCGGCTGTCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG  
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGACAGTGCAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC  
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCT  
GGGGTCTTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC  
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAG  
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC  
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC  
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG  
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAAATAAAAATGAAACGTG

## **FIGURE 217**

MRGSQEVLMMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPKGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

109101"44582660

# FIGURE 218

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGTGAGGAGGAGACAGCCTCCCGGCCCGGGGAG  
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCTGCGGTGAGCTGCCGGCCG  
AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGG  
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT  
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGAATCGCAAAACCCATTTTGGAGCAGGAATCCAATCA  
TGTCTGTGATGGTGGTGAGAAAGAGGTGACACGAAATGGGAGAAACTCCCAGGCAGGAACACCTTTTGCTGTG  
ATGGCCCGCTCATGATGGCCCCGGCAAAAGGGCATTTTCTACCTGACCTTTTCTCATCTCTGGGGACATGTACAC  
TCTTCTTCGCCCTTTGAGTGCCGCTACCTGGCTGTTGAGCTGTCTCTGCCATCCCTGTATTTGCTGCCATGCTCT  
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCTGGAGTGATTCTCGGGCGCTACCAGATG  
AAGCAGCTTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGCCTCGTA  
TCAAGAATTTCCAGATAAACCAACCAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCCGGCCTCCCC  
GGGCCTCCCATTGCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTG  
TTGGAAAGAGGAACCTACCGCTACTTCTACCTTTCATCCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCCCT  
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAAATTGGCTTCTTGAGACATTGAAAGAAACTCCTGGAAGTGT  
TTCTAGAAGTCCCTCATTTGCTTCTTTACACTCTGGTCCGTCTGCGGACTGACTGGATTTTCACTTTTCTCGTGG  
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC  
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGGCCCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA  
TTTTGCCACTGGAGGAAAGTGAAGTCGACCTCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC  
CAGCCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG  
AGCCCCCAGAGCCACCACAGGAGGAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTGTGT  
TAATTAGGGCTATGAGAGATTTAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT  
GTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAAC  
CAAGGCAGTGGCAGAAGATGTCAGTCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT  
CCATGGCCTCAGCCACAGGGTCCCCCTTGAGCCCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTCAC  
TGGTCTCATTCTGGGGCTAAAAGTTTGTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA  
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG  
TGGGGTCAGAAGATTTCTCTGGCCACCAAGTGCCAGCATTGCCCCACAAATCCTTTTAGGAATGGGACAGGTACCT  
TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCTTTTGACTCCTGCTCCCATTAGGAG  
CAGGAATGGCAGTAATAAAAAGTCTGCACCTTTGGTCATTTCTTTTCTCAGAGGAAGCCCGAGTGCTCACTTAAAC  
ACTATCCCCCTCAGACTCCCTGTGTGAGGCCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG  
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCTCAAATAAAAAAAAAAATGCTAACCAGTTCTTCCATTAGCCCT  
CGGCTGAGTGAGGGAAAGCCAGCACTGCTGCCCTCTCGGGTAACCTACCCCTAAGGCCTCGGCCCCACCTCTGGCT  
ATGGTAACCACACTGGGGGCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTT  
CACCTTGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTTCAAGGAAGAAGATTTATGT  
ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT  
GCGGTGGGGAGTGTAACCGGAACCTTTTCATCTATTTGAAGGCGATTAACTGTGTCTAATGCA

097452660

## **FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGFYLTFLILGTCTLFFAFECRYLAV  
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNYRYFYL  
FILSLSLLLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLI CFFTLWSVVGLTGFHTF  
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPEPPQEAAEAEK

**Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

0997944-10501  
T09T0T-44582660



## **FIGURE 220**

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT  
CCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA  
ACATCGT

099758/660

## FIGURE 221

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATTGTAGAGATTTCT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTACCGTGAACCTATCCACCATA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA  
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

097844101901

## **FIGURE 222**

MKTIQPKMHNSISWAIIFTGLAALCLFQGVVRSGLATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYECASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGTQCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNITCVASNKLGHNTNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLLKF

**Signal peptide:**

amino acids 1-28

09584-101

## **FIGURE 223**

GAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT  
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCAAAATTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG

## FIGURE 224

ATGGCTGGTGACGGCGGGGCGGGGACCGGGGCGCGGCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA  
ATCACCGCCTGGCCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG  
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT  
GCACTGCTTCTGGGCTGCCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCCTTACA  
GAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC  
CAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC  
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAGAACACACCTTCAACTCCAGCAGTGAAGCTGAG  
CAGAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGA  
GACCTCATTGAGAAGATTGGTGGTTGGAAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG  
GCAGTAGCAGGGACCTACAGGGCCACCCATTCTTACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC  
AATGTTATCCAGGTGGACAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAAGTGCCAATGAG  
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG  
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGCGCGAC  
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC  
CTGTCTTTCTTGCTGTCAACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG  
CAGGTGTCAAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG  
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTCTATGGCACTAAGAAG  
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC  
GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG  
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT  
GATATGATTGGTTTCCAGACTTTATCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT  
GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACCTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG  
CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC  
GTCTTCCCCGCTGGCATCCTGCAGGCCCTTCTATGCCCGCAACCAACCCCAAGGCCCTGAACCTCGGTGGCATC  
GGTGTGGTCAATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG  
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACGGCCTGCATGGAGGAACAGTACAATCAA  
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG  
GCTGCCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC  
AACCACCAGCTCTTCTCGTGGGATTTGCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG  
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCTTCCG  
CACTTCGGCTGCCCTGTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTTAGACCTGGATCAGGGGA  
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCTGACAAAGCTGTTTGCTCTTGGGTGGGAGGAAGCAA  
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG  
TGCTCTGCTTTGGGGGTGCCCTGCCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTACCCCT  
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

## **FIGURE 225**

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDP SH  
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA  
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN  
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLFLPSRDYYLNRTANEKVLTA Y  
LDYMEELGMLLGGRPTSTREQMQQVLELEIQ LANITVPQDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLELSDSEPVVVGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLL ETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI  
SEIRTA FEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF  
FQNMNLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH  
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS  
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNP GQLCEVW

**Type II Transmembrane domain:**

amino acids 32-57

## FIGURE 226

GCCCCGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCCGCTCCCGCGCCCTCCTCCCTCCCTCCTCCC  
CAGCTGTCCCGTTTCGCGTCATGCCGAGCCTCCCGGCCCGCGCGCCCGCTGCTGCTCCTCGGGCTGCTGCTGCT  
CGGCTCCCGGCCGCGCGCGCGCGCCAGAGCCCCCGTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCC  
CGTTCGGGGAGCGGCAGGTAGGTGGGCGCCCCGGGGAGGCGCGGGCGGGGAGTCCGGGCTCGGGGCGAGTCAGCGC  
CAGCCCGAGGGGGCGCGGGGCGCAGGTGGCTCGGCGCGGCGGGCGGCCCGAGGGTGGGCGGGGCGAGAAGGSC  
GCGGTGCCTGGGACCCGGGACCCGCGGGCAGCCCCCGGGGCGGCACACGGCGCGAGCTGGGCAGCGGCCTCCAGC  
CAAGCCCGTCCCCGAGGCTGCACCTTCGGCGGGAAGGTCTATGCCCTTGACGAGACGTGGCACCCCGACCTAGG  
GGAGCCATTTCGGGGTGATGCGCTGCGTGTGTGCGCTGCGAGGCGCAGTGGGGTGCCTGTACCAGGGGCCCTGG  
CAGGGTCAGCTGCAAGAACATCAAACCAGAGTGCACCAACCCCGGCTGTGGGCGAGCCGCGCCAGCTGCCGGGACA  
CTGCTGCCAGACCTGCCCCAGGACTTCGTGGCGCTGTGTACAGGGCCGAGGTGCGCAGGCGGTGGCACAGACCCG  
AGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCTACAGGCGGCTGGACCGCCCTACCAGGATCCGCTT  
CTCAGACTCCAATGGCAGTGTCTGTGTTGAGCACCTGACGCCCCACCAAGATGGCCTGGTCTGTGGGGTGTG  
CGGGGCGAGTGCCTCGGTTGTCTGTGCGGCTCCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCA  
CCCTTCAGGGGAGGTCTGGGGGCTCTCATCCGGCACCGGGCCCTGTCCCCAGAGACCTTCAGTGCCATCCTGAC  
TCTAGAAGGCCCCACCAGCAGGGCGTAGGGGGCATCACCTGCTCACTCTCAGTGACACAGAGGACTCCTTGCA  
TTTTTTGCTGCTCTTCCGAGGCCCTTGACAGGACTAACCCAGGTTCCCTTGAGGCTCCAGATTCTACACAGGGGCA  
GCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCAGGAACAGGCTTTGCTGAGGTGCTGCCAACCTGACAGT  
CCAGGAGATGGACTGGCTGGTGTGCTGGGGGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCAT  
CAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGTCCTGCAAGTGTCTTTGTGGGGCTAATGCCCTGATCCC  
AGTCCAAACGGGTGCTGCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCTGATCCTCCAGGTGCAATT  
GGTAGGGACAACAGTGAGGTGGTGGCCATGACACTGGAAACCAAGCTCAGCGGAGGGATCAGCCACTGTCTCT  
GTGCCACATGGCTGGCCTATCCTCCCCGCCCCAGGCCGTGGGTATCTGCCCTGGGCTGGGGTGGCCGAGGGG  
TCATATGCTGCTGCAGAAATGAGCTCTTCTGAACGTGGGCACCAAGGACTTCCCAGACGGAGAGCTTCGGGGGCA  
ACGTGGCTGCCCTGCCCTACTGTGGGGCATAGCGCCCGCCTGCCCGTGGCCCTAGCAGGAGCCCTGGTGTACCC  
CCCTGTGAAGAGCCAAGCAGCAGGGCACGCTGGCTTTCCTTGAGTACCCACTGTCACTGCACTATGAAGTGCT  
GCTGGCTGGGCTTGGTGGCTCAGAACAGGCACTGTCACTGCCACCTCCTTGGGCTCCTGGAACGCCAGGGG  
TCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAGGCCAGGGTGTGGTGAAGGACCTGGAGCCGGAAGTGTGCG  
GCACCTGGCAAAAGGCATGGCTTCCCTGATGATCACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGGAGCCT  
CTCCTCCCAGGTGCATAGCCAACCAATGTGAGGTGGCGGACTGCGCCTGGAGGCGGCCGGGGCCGAGGGGGT  
GCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCTGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGC  
CAAACCTGGTGGTCTTGGGCGGCCCGAGACCCCAACACATGCTTCTTCGAGGGGCGAGCAGCGCCCCACGGGGC  
TCGCTGGGCGGCCAACTACGACCCGCTCTGCTCACTGCACTGCCAGAGACGAACGGTGTCTGTGACCCGGT  
GGTGTGCCACCGCCAGCTGCCCAACCCGGTGCAGGCTCCCGACCAAGTGTCTGCCCTGTTTGGCTGGCTGCTA  
TTTTGATGGTGACCGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCCTTTGGCTTAATTA  
GTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCACTGTCCCCGGCTGGC  
CTGTGCCCAGCCTGTGCGTGTCAACCCCAACCGACTGCTGCAACAGTGTCCAGGTGAGGCCACCCCGAGCTGGG  
GGACCCCATGCAAGGCTGATGGGCCCCGGGGCTGCCGTTTGTGTTGGGAGTGGTTCCAGAGAGTCAAGAGCTGGCA  
CCCTCAGTGTCCCCGTTTGGAGAGATGATGACCTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGT  
GTGAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGAGAGCTTCCAGGGAGGTCCCTGAAGAAGCTGAAGGTCA  
CTGTGTCCAGTGCCTCTGGGGGACACTCAGTGTCTGCTGTCTTGTACCAGGCAGGGGTGCGCTCCTGATCAG  
GGGATGACTGTCTACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTGCATGCTGTTCCCGCTGCACGGGCCACC  
GGCGGCGTAAGTGAGGGAGTCCAGGGTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAG  
GGAAGGGAGCACTCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAATCCACCCTCACAGCA  
ACCTGGTGGAAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGAAATTAAGCAACGAG  
ATGAAGGTCAACCAGCTGTGTGCACTGACCTGTTTAGAAAATACTGGCCTTTCTGGGACCAAGGCAGGGATGCTT  
TGCCCTGCCCTCTATGCCCTCTGTGCTCTCCACTCCCTCTCCCTCCTCCAACATTCCTCCTCTCTGTCTCC  
AGCAGCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCC  
AAGTGACCAAGAGGATGGGGCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCACTTCTCCTGTGGGAAG  
GCCAGTGCCCTTGTCTCTGTCTGCTCTACTCCCAACCCCACTACCTCTGGGAACCAAGCTCCACAAGGGG  
GAGAGGCACTGGGGCCAGACCGAGGTACAGCCACTCAAGTCTGCCCTGCCACCCTCGGCCCTGTCTCTGGAA  
GCCCCACCCCTTTCTTCTGTACATAATGTCACTGGCTTGTGGGATTTTAAATTTATCTTCACTCAGCACCAG  
GGCCCCGGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTGTATTTATTAAGAAC  
ATTTCTTTTTTCAGTCTTTGGGCATGAGGTTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCTGGTGGAGAAGGG  
GCNGAGAGTAGGAGGTGAGAGAGAGGAGCTCTGACACTTGGGGAGCTGAAAGAGACCTGGAGAGGCAGAGGATAG  
CGTGGCCTTTGGCTGGCATNCTGGGTTCCGACAGAGGGGCTGGGGATGGTTCTTGAGATGGTCTAGAGACTCAAG  
AATTTAGGGGAAGTAGAAGCAGGATTTTGAAGTCTCAAGTTTAGTTTCCACATCGCTGGCCTGTTGTGCTGACTTCATG  
TTTGAAGTTGCTCCAGAGAGAGAATCAAAGGTGTCAACAGCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTCT  
TTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC

## **FIGURE 227**

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA  
CCGGGGCCGCGGGCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCCGAC  
TCCACCATGAACGTGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTCTGGA  
GGAACCCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG  
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTCCTTAC  
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG  
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAACTGCCCCCT  
CCTTTCTTTCTTCTTTTCTTCCCTCCCTCCCTTTTCTTCCCCTTTTCTTCCCTTCTTCCCTTCC  
TCTTATTCTTCTAGTAGGTTTCTATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCTG  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTTCAGTGTGATGGGTTTCATGGACCT  
AGATAGGCTGATAACAAAGCTCACAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC  
AGCAAAGTCTTCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG



## FIGURE 228

ATGCCTACTACCTTCCAATAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC  
TTCTATGCCCCGAACCAACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA  
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC  
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG  
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCGCTTCCGCGTGTCTGGGCACCTCTCTCCAACCTCCCGTGACTTCCTGCGGC  
ACTTCGGCTGCCCTGTCTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGTCAACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT  
TTGCTCTTGGGTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA  
GGTGACATGAGTACAGACCCTCCTCAATCACACATTGTGCCTCTGCTTTGGGGGTGCCCCCT  
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCAACCCTGCCTGGAAGAG  
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT  
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG  
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC  
TGGCTCACCTCACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCAGTG  
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC  
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGATATGTGTAGCGGGTACTGGTTCCCTGT  
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA  
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC

CCCTTTGGGGGTGCCCCCT

## FIGURE 229

CCCACGCGTCCGAGCCGCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA  
GGAGGGGAGGCAAAAACACCGAAAAACAAAAGAGAGAAACAACACCCAACAACCTGGGGTGG  
GGGGAAGAAAGAAAGAAAAGAAACCCACCCACCCACCAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG  
TGGGGGAGTGCGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG  
CTGTTGGTGACAGGGTGCTTGTTCGCTCGAACCAAGTGGCTGGCGGCGGTGCTCCTCAGCCTGTG  
CTGCCTGCTACCTCCTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCTGGGCGGCCGTGG  
ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT  
TCAAAGGGTGCTGGCTGAACCGGTCAAGTATTATTTTTCGCGGAGGTGATAAGTGGTCAGT  
GGATCCTCGAGTTTCAATTTCAACATTTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG  
TAGATGTGACAGATGATGGCCATACACGTGTTCTGTTTCACTCAACATACACCCAGAACA  
ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC  
CGTCAATGAAGGAACCAACGTCACTCTTACTTGTTCGCGCACTGGGAAACCAGAGCCTTCCA  
TTTCTTGGCGACACATCTCCCATCAGCAAAACCATTGAAAATGGACAATATTTGGACATT  
TATGGAATTACAAGGGACCAGGCTGGGGAATATGAATGCAGTGCAGGAAATGCTGTGTGATT  
CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTAGGAAATTAAAT  
CTGGCACCGTGACCCCCGGACGCAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT  
CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTAT  
TCAAAATTTTAGCACAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTTCGGCA  
ATTATACCTGTGTGGCTGCCAACAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCCT  
CCAAGTACAGCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT  
TGTGTTGACACTGTCTCTTTTACCAGCATATTCTACCTGAAGAATGCCATTCTACAATAAA  
TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT  
GGTACAGTTTGTAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC  
TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTCTACTCTTTTTTTGATTAGCTACATTA  
CCTTGTGAAGCAGTACACATTGTCTTTTAAAGACGTGAAAGCTCTGAAATTACTTTTAG  
AGGATATTAATTGTGATTTCATGTTTGTAACTTACAACCTTTCAAAGCATTAGTCATGGT  
CTGCTAGGTTGCAGGCTGTAGTTTACAAAACGAATATTGCAGTGAATATGTGATTCTTTAA  
GGCTGCAATACAAGCATTAGTTCCTGTTTCAATAAGAGTCAATCCACATTTACAAAGATG  
CATTTTTTTCTTTTTTGATAAAAAAGCAAATAATATTGCCCTCAGATTATTTCTTCAAATA  
TAACACATATCTAGATTTTCTGCTTGCATGATATTAGGTTTCAGGAATGAGCCTTGTAAT  
ATAACTGGCTGTGCAGCTCTGCTTCTCTTTCTGTAAGTTCAGCATGGGTGTGCCTTCATAC  
AATAATATTTTTCTCTTTGTCTCCAATAATATAAAATGTTTTGCTAAATCTTACAATTTGA  
AAGTAAAAATAAACCAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC  
TATTGGACTGTAAAAATCTCTTCTGCACTGACAATGGGGTTTGAGAATTTTGCCCCACACT  
AACTCAGTTCCTTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATATGATTTCT  
TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCTTTTAAATGACAGCACA  
GTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCTTTTCACTAGTCCAAGCCAAAAA  
TTTTAAGATGATTTGTGAGAAAGGGCACAAAGTCTATCACCTAATATTACAAGAGTTGGTA  
AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGTATGGA  
TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC  
AGGAGGAAATTACAGAGACAATTATGACAACTGAAATGAGACATGCACATAATATAGATACA  
CAAGGAATAATTTCTGATCCAGGATCGTCCTTCAAATGGCTGTATTTATAAAGGTTTTTGG  
AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTTAAATTGACCTGCCA  
AGGTAGCTGAAGACCTTTTAGACAGTTCATCTTTTTTTTTTAAATTTTTTCTGCCTATTTAA  
AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 230**

MMLLVQGACCSNQWLA AVL LLSLCCLLPSCLPAGQSVDFPWA AVDNMMVRKGDTAVLR CYLED  
GASKGAWLNRSSII FAGGDKWSVDPRVSISTLNKRDYSLQIQNV DVTDDGPYTCSVQTQHTP  
RTMQVHLTVQVPPKIYDISNDMTVNEG TNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL  
DIYGITRDQAGEYECSAENAVSFPDVRKVKV VVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV  
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILT VTNVTQEHFGNYTCVAANKLGTTNASLPL  
NPPSTAQYGITGSADVLFSCWYLVLTLS SFTSIFYLK NAILQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 326-345

**N-glycosylation sites.**

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

**Casein kinase II phosphorylation site.**

amino acids 147-151, 208-212, 224-228

**Tyrosine kinase phosphorylation site.**

amino acids 178-186

**N-myristoylation sites.**

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,  
302-308, 319-325

**Myelin P0 protein:**

amino acids 92-121

## FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGG  
CTCCAGGACTTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA  
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTACCAAATTGCAATGGAGCCTTTCGAAA  
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATC  
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC  
GCGGCTCCGGGTCTTGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT  
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG  
CAAGTCCTGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT  
AGACAACCTTCACTCAGAACCCAGGGATGTTTCAAGATCAAAGGTGAACAAGGCGCCCCAGGTC  
TTCAAGGTCACAAGGGGGCCATGGGCATGCCTGGTGCCCCTGGCCCGCCGGGACCACCTGCT  
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG  
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCCAGGGTGCTCCAGGGAAGCAAG  
GAGCCACTGGCACCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT  
GGCCCAAAGGGGAAACTGGAACCTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA  
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGAGGGCCTCCTGGAGCCCAGGGGAGTA  
AAGGTGACTTCGGGAGGCCAGGCCCACCAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGAT  
CAAGGACAACCTGGACTGCAGGGTGTTCGGGGCCCTCCTGGTGAGTGGGACACCAGGTGC  
CAAGGGTGAGCCTGGCAGTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA  
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA  
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG  
GCTGGCAGGTCCCAAGGGAGCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG  
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC  
GTCAGGATTGTCGGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG  
GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT  
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT  
GTTCAAGTGTGCGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA  
TGACTGCAGCCACGAGGAGGACGAGGCGTGGAGTGCAGCGTCTGACCCCGGAAACCCTTTCA  
CTTCTCTGCTCCCGAGGTGTCCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT  
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAAATAAGCTCAACATCATTGA

## **FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAFHQIAMEPF EINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL  
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR  
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD  
GATGPSGPQGPPGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE  
KGDGLPLPGSKGDRGMKGDAGVMGPPGAQGSKGDGFRPGPPGLAGFPGAKGDQGPGLQGVPG  
PPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTLQGQQGRKGESGVPGPA  
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGR  
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLW  
SCTKNSWGHHDCSHEEDAGVECSV

### **Transmembrane domain:**

amino acids 47-66 (type II)

### **N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

### **Tyrosine kinase phosphorylation site.**

amino acids 432-440

### **N-myristoylation sites.**

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521

### **Amidation site.**

amino acids 360-364

### **Leucine zipper pattern.**

amino acids 56-78

### **Speract receptor repeat**

amino acids 422-471, 488-519

### **Clq domain proteins.**

amino acids 151-184, 301-334, 316-349

109707 44582660

## **FIGURE 233**

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT  
CTTCTCCTTTTGCCCAAACACACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG  
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTTCAC  
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA  
GAAAGATACTAAAAGATCACAACTGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG  
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG  
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTTCG  
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTTC  
CCACAAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT  
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA  
AGTTAATTCAATCTAAAAAAAAAAAAA

109101"4453.660

## **FIGURE 234**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLGVQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG

KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 72-76

**Tyrosine kinase phosphorylation site.**

amino acids 63-71

FIGURE 234

## FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCCAGGTCTGGAGCGAATTCAGCCTGCAGGG  
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGC  
 GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCAGGAGGCGGGCTCTGCTCGCGCCGAGATG  
 TGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCGCGCTGGCTGTG  
 CGCTGGGGCGCTGGTGTGCTGGCGGGTGGCTTCTTTCTCCTCGGCTTCCTCTTCGGGTGGTTTA  
 TAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTTGGAT  
 GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC  
 AGGAACAGAACAAAACCTTTCAGCTTGCAAAGCAAATTCATCCCAGTGGAAGAATTTGGCC  
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCTGTTGTCCTACCCAAATAAGACTCATCCC  
 AACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTATTTGAACC  
 ACCTCCTCCAGGATATGAAAATGTTTTCGGATATTGTACCACCTTTCAGTGCTTTCTCTCCTC  
 AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAA  
 TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGT  
 TTTTCAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT  
 CCGACCCTGCTGACTACTTTGCTCCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTTCCT  
 GGAGGTGGTGTCCAGCGTGGAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACC  
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAA  
 GTATTCCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC  
 TCAGCACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG  
 CTTTACTGGAACTTTTTCTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA  
 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGAACCAGACAGATATGTCATT  
 CTGGGAGGTCAACGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGT  
 TGTTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA  
 CAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA  
 GAGGAGAATTCAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT  
 AGAAGGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC  
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG  
 ACTAAAAAAGTCTTTCCCCAGAGTTTCACTGGCATGCCAGGATAAGCAAATTTGGGATCTGG  
 AAATGATTTTGAAGGTGTTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGCACGGTATACTA  
 AAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT  
 GAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCCAGGTTTCG  
 AGGAGGGATGGTGTGTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGATTGTGAGATTATG  
 CTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA  
 ATGAAGACATACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT  
 TGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAA  
 TGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTTTATTGATCCATTAGGGTTACCAGAC  
 AGGCCTTTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC  
 ATTCCCAGGAATTTATGATGCTCTGTTTGAATTTGAAAGCAAAGTGGACCCTTCCAAGGCCT  
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACT  
 TTGAGTGAAGTAGCCTAAGAGGATTTTTTATAGAGAATCCGTATTGAATTTGTGTGGTATGTCA  
 CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAAATTGGTATATTTGAAATAAAGT  
 TGAATATTATATATAA



## FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFL  
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH  
PNYISIINEDGNEIFNTSLFEP PPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF  
KLERDMKINCSGKIVARYGKVFRGNKVNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL  
PGGGVQRGNIILNLNGAGDPLTPGYPANAYRRGIAEAVGLPSIPVHPIGYYDAQKLEKMG  
GSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKV KMHISTNEVTRIYNVIGTLRGAVEPDRYV  
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW  
AEENSRLQERG VAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYES  
WTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET  
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ  
EMKTYSVSFDLSFSAVKNFTEIASKF SERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP  
DRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVQRQIYVAAFTVQAAAE  
TLSEVA

### **Signal sequence:**

amino acids 1-40

### **N-glycosylation sites.**

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,  
459-463, 476-480, 638-642

### **Tyrosine kinase phosphorylation sites.**

amino acids 363-372, 605-613, 606-613, 617-626

### **N-myristoylation sites.**

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,  
360-366, 427-433, 529-535, 707-713